



Thu Feb 27 09:12:57 2003

```
QY 8 GRGKCPSPNEIFSRCDGRQCFPCPNVVPKPLCIKICAPGCVCVR 49
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 4 GSKCKN----CRKRS-CRKSCCSCCPAG--CNNCARGCVCK 38

RESULT 3
A42040
kalitoxin 1 [validated] - scorpion (Androctonus mauretanicus)
N:Alternate names: KTX1
C:Species: Androctonus mauretanicus mauretanicus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Sep-2000
C:Accession: A42040
R:Crest, M.; Jacquet, G.; Gola, M.; Zerrouk, H.; Benslimane, A.; Rochat, H.; Mansuelle,
J. Biol. Chem. 267, 1640-1647, 1992
A:Title: Kalitoxin, a novel peptidyl inhibitor of neuronal BK-type Ca(2+)-activated K+
A:Reference number: A42040; MUID:92112881; PMID:1730708
A:Accession: A42040
A:Molecule type: protein
A:Residues: 1-37 <CRE>
A:Note: sequence extracted from NCBI backbone (NCBIP:76008); conformation and disulfide
R:Fernandez, I.; Romi, R.; Szendefi, S.; Martin-reaucalire, M.F.; Rochat, H.; Van Rietsch
submitted to the Brookhaven Protein Data Bank, June 1994
A:Reference number: A67062; PDB:1KTX
A:Contents: annotation; conformation by (1)H-NMR, residues 1-37
C:Comment: This toxin inhibits neuronal BK-type calcium-activated potassium channels.
C:Superfamily: kalitoxin
C:Keywords: neurotoxin; potassium channel inhibitor; venom
F:8-28,14-33,18-35/Disulfide bonds: #status experimental
Query Match 12.3%; Score 48; DB 2; Length 37;
Best Local Similarity 29.8%; Pred. No. 2.4e+02;
Matches 14; Conservative 4; Mismatches 17; Indels 12; Gaps 2;

QY 16 EIFSRCDGRQCFPCPNVVPKPLCIKICAPGCVCRLGYLRNKKKVCVP 62
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 3 EINVKCSG-----SPOCLPKCKDAGM-RFGKCMNRKCHCTP 37

RESULT 4
A47753
beta-defensin-10 - bovine
N:Alternate names: peptide BNRD-10
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C:Accession: A47753
R:Seasted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A:Title: Purification, primary structures, and antibacterial activities of beta-defensin
A:Reference number: A45495; MUID:93203264; PMID:8454635
A:Accession: A47753
A:Molecule type: protein
A:Residues: 1-40 <SEL>
A:Note: sequence modified after extraction from NCBI backbone
C:Keywords: antibacterial; disulfide bond; pyroglutamic acid
F:1-40/Product: beta-defensin-10 #status experimental <MAL>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9-38,16-31,21-39/Disulfide bonds: #status predicted
Query Match 12.3%; Score 48; DB 2; Length 40;
Best Local Similarity 29.4%; Pred. No. 2.5e+02;
Matches 10; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 7 GGRGKCPSPNEIFSRCDGRQCFPCPNVVPKPLCIK 40
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 11 GNRGTC----LLNRCPRGRMRQIGTCLAPRVKCCR 40

RESULT 5
C54471
agitoxin 3 - scorpion (Leiurus quinquestriatus)
N:Alternate names: AGTX-3
C:Species: Leiurus quinquestriatus hebraeus
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 23-May-1997

C:Accession: C54471
R:Garcia, M.L.; Garcia-Calvo, M.; Hidalgo, P.; Lee, A.; MacKinnon, R.
Biochemistry 33, 6834-6839, 1994
A:Title: Purification and characterization of three inhibitors of voltage-dependent K
A:Reference number: A54471; MUID:94263998; PMID:8204618
A:Accession: C54471
A:Molecule type: protein
A:Residues: 1-38 <GAR>
C:Superfamily: kalitoxin
C:Keywords: neurotoxin; potassium channel inhibitor; venom
F:8-28,14-33,18-35/Disulfide bonds: #status predicted
Query Match 12.0%; Score 47; DB 2; Length 38;
Best Local Similarity 37.8%; Pred. No. 3e+02;
Matches 14; Conservative 3; Mismatches 16; Indels 4; Gaps 2;

QY 30 PNVVP---KPLCIKICAPGCVCRLGYLRNKKKVCVR 63
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 3 PINVPTGSPQCIKPKCKDAGM-RFGKCMNRKCHCTPK 38

RESULT 6
B54471
agitoxin 2 - scorpion (Leiurus quinquestriatus)
N:Alternate names: AGTX-2
C:Species: Leiurus quinquestriatus hebraeus
C>Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 23-May-1997
C:Accession: B54471
R:Garcia, M.L.; Garcia-Calvo, M.; Hidalgo, P.; Lee, A.; MacKinnon, R.
Biochemistry 33, 6834-6839, 1994
A:Title: Purification and characterization of three inhibitors of voltage-dependent K
A:Reference number: A54471; MUID:94263998; PMID:8204618
A:Accession: B54471
A:Molecule type: protein
A:Residues: 1-38 <GAR>
C:Superfamily: kalitoxin
C:Keywords: neurotoxin; potassium channel inhibitor; venom
F:8-28,14-33,18-35/Disulfide bonds: #status predicted
Query Match 11.9%; Score 46.5; DB 2; Length 38;
Best Local Similarity 39.3%; Pred. No. 3.4e+02;
Matches 11; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 36 PLCIKICAPGCVCRLGYLRNKKKVCVR 63
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 12 PQCIKPKCKDAGM-RFGKCMNRKCHCTPK 38

RESULT 7
S18174
metallothionein - common bobwhite (fragment)
C:Species: Colinus virginianus (common bobwhite)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S33379; S18174
R:Shartzer, K.L.; Kage, K.; Sobleski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A:Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey meta
A:Reference number: S33378; MUID:93247066; PMID:8483164
A:Accession: S33379
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-43 <SHA>
A:Cross-references: EMBL:X62512; NID:962751; PIDN:CAA44371.1; PID:962752
C:Superfamily: metallothionein
Query Match 11.9%; Score 46.5; DB 2; Length 43;
Best Local Similarity 31.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 5; Mismatches 17; Indels 7; Gaps 3;

QY 8 GRGKCPSPNEIFSRCDGRQCFPCPNVVPKPLCIKICAPGCVCVR 49
  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 4 GSKCKN----CRKRS-CRKSCCSCCPAG--CNNCARGCVCK 38
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## RESULT 8

S43283  
gallinacin - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999  
C:Accession: S43283  
R:Harwig, S.S.L.; Swiderski, K.M.; Kokryakov, V.N.; Tan, L.; Lee, T.D.; Panyutich, E.A.;  
FEBS Lett. 342, 281-285, 1994  
A:Title: Gallinacins: cysteine-rich antimicrobial peptides of chicken leukocytes.  
A:Reference number: S43282; MUID:94200386; PMID:8150085  
A:Accession: S43283  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-39 <VAR>

I48887

cryptdin-4 - mouse (fragment)  
 N:Alternate names: crypt defensin 4  
 C:Species: Mus musculus (house mouse)  
 C:Date: 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 16-Jul-1999  
 C:Accession: I48887; D43279  
 R:Huttner, K.M.; Selsted, M.E.; Ouellette, A.J.  
 Genomics 19, 448-453, 1994  
 A:Title: Structure and diversity of the murine cryptdin gene family.  
 A:Reference number: A50017; MUID:94245232; PMID:8189287  
 A:Accession: I48887  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-34 <RES>  
 A:Cross-references: EMBL:U03032; NID:9437245; PIDN:AAA57172.1; PID:9437246  
 R:Selsted, M.E.; Miller, S.I.; Henschen, A.H.; Ouellette, A.J.  
 J. Cell Biol. 118, 929-936, 1992  
 A:Title: Enteric defensins: antibiotic peptide components of intestinal host defense.  
 A:Reference number: A43279; MUID:92363933; PMID:1500431  
 A:Accession: D43279  
 A:Molecule type: protein  
 A:Residues: 3-33 <SEL>  
 A:Experimental source: intestinal epithelium  
 A:Note: sequence extracted from NCBI backbone (NCBIP:110696)  
 C:Genetics:  
 A:Gene: Defc4  
 C:Superfamily: mammalian defensin

Query Match 10.6%; Score 41.5; DB 2; Length 34;  
 Best Local Similarity 36.4%; Pred. No. 9.6e+02;  
 Matches 8; Conservative 4; Mismatches 7; Indels 3; Gaps 1;  
 QY 46 CVCRLGLYLRNKKKVCVPRSKCG 67  
 | | | | | : : : : : | | |  
 Db 6 CYCRKGCHCKRGERV---RGTCG 24

RESULT 14

SMFF2

metallothionein 2 - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 24-Nov-1999  
 C:Accession: S14706; A38808; A29863; S10476  
 R:Sillar, P.; Theodore, L.; Mokdad, R.; Erraiss, N.E.; Cadic, A.; Wegnez, M.  
 J. Mol. Biol. 215, 217-224, 1990  
 A:Title: Metallothionein Mto gene of Drosophila melanogaster: structure and regulation.  
 A:Reference number: S14706; MUID:91012582; PMID:1976815  
 A:Accession: S14706  
 A:Molecule type: DNA  
 A:Residues: 1-43 <STL1>  
 A:Cross-references: EMBL:X52098; NID:g8274; PIDN:CAA36318.1; PID:g295751  
 A:Accession: A38808  
 A:Molecule type: protein  
 A:Residues: 'X', 3-24, 'X', 26-27 <STL2>  
 A:Note: 15-Thr was also found  
 R:Mokdad, R.; Debec, A.; Wegnez, M.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 2658-2662, 1987  
 A:Title: Metallothionein genes in Drosophila melanogaster constitute a dual system.  
 A:Reference number: A29863; MUID:87204190; PMID:3106973  
 A:Accession: A29863  
 A:Molecule type: mRNA  
 A:Residues: 1-43 <MOK>  
 A:Cross-references: GB:M16250; NID:g157884; PIDN:AAA28683.1; PID:g157885  
 C:Genetics:  
 A:Gene: Mto  
 A:Cross-references: FlyBase:FBgn0002869  
 A:Map position: 3R 92E  
 A:Introns: 9/1  
 C:Superfamily: metallothionein  
 C:Keywords: blocked amino end; chelation; metal binding  
 F:1/Modified site: blocked amino end (Met) #status experimental  
 Query Match 10.6%; Score 41.5; DB 1; Length 43;

Best Local Similarity 22.6%; Pred. No. 1.1e+03;

Matches 14; Conservative 6; Mismatches 15; Indels 27; Gaps 4;

QY 5 GLGGRGKCPSENFPSRCDGRCQRCFPCNVVFKPLCIKICAGCVCVRLGLYLRNKKKVCVPRS 64

| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : |

Db 5 GCGTNCQCSA-----QKCGDNC-----ACNKDCQ--CVCKNG-----PKD 37

QY 65 KC 66

| |

Db 38 QC 39

RESULT 15

T12322

metallothionein - common ice plant  
 C:Species: Mesembryanthemum crystallinum (common ice plant)  
 C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 20-Apr-2000  
 C:Accession: T12322  
 R:Michalowski, C.B.; Bohnert, H.J.  
 submitted to the EMBL Data Library, June 1998  
 A:Description: A metallothionein homolog from the ice plant Mesembryanthemum crystallinum  
 A:Reference number: Z17492  
 A:Accession: T12322  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-45 <MIC>  
 A:Cross-references: EMBL:AF078911; NID:g3342195; PID:g3342196  
 C:Keywords: metal binding

Query Match 10.6%; Score 41.5; DB 2; Length 45;

Best Local Similarity 38.5%; Pred. No. 1.2e+03;

Matches 10; Conservative 1; Mismatches 10; Indels 5; Gaps 2;

QY 42 CAPGCVRLGLYLRNKKKVCVPRSKCG 67

| | | | | : : : : : | | | | | : : : : : |

Db 15 CGSGCNCNRSYAK-KDDGC-----KCG 35

RESULT 16

S74088

defensin - Mediterranean mussel  
 C:Species: Mytilus galloprovincialis (Mediterranean mussel)  
 C:Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 04-Feb-2000  
 C:Accession: S74088  
 R:Hubert, F.; Noel, T.; Roch, P.  
 Eur. J. Biochem. 240, 302-306, 1996  
 A:Title: A member of the arthropod defensin family from edible Mediterranean mussels  
 A:Reference number: S74088; MUID:97025339; PMID:8925841  
 A:Accession: S74088  
 A:Molecule type: protein  
 A:Residues: 1-38 <HUB>  
 A:Experimental source: hemolymph  
 C:Keywords: antibiotic  
 F:4-25,10-33,14-35,21-38/Disulfide bonds: #status predicted

Query Match 10.4%; Score 40.5; DB 2; Length 38;

Best Local Similarity 34.4%; Pred. No. 1.3e+03;

Matches 11; Conservative 3; Mismatches 7; Indels 11; Gaps 3;

QY 2 GFGGLGGRGKCPSPN-EIFSR-----DGRQRCFC 29

| | | | | : : : : : | | | | | : : : : : |

Db 1 GFG-----CPNNYQCHRHCKSIPIRCGGYC 25

RESULT 17

B32038

mu-agatoxin II - funnel-weaving spider (Agelenopsis aperta)  
 C:Species: Agelenopsis aperta  
 C:Date: 31-Jul-1989 #sequence\_revision 22-Jul-1994 #text\_change 15-Oct-1996  
 C:Accession: B32038  
 R:Skinner, W.S.; Adams, M.E.; Quistad, G.B.; Kataoka, H.; Cesarin, B.J.; Enderlin, F.  
 J. Biol. Chem. 264, 2150-2155, 1989  
 A:Title: Purification and characterization of two classes of neurotoxins from the fun

A:Reference number: A32038; MUID:89123282; PMID:2914898

A:Accession: B32038  
A:Molecule type: protein  
A:Residues: 1-37 <SKI>  
C:Comment: mu-agatoxins cause paralysis in insects by activating neuronal sodium channel  
C:Superfamily: curatotoxin  
C:Keywords: amidated carboxyl end; myotoxin; venom  
F:2-17,9-23,18-33,25-31/Disulfide bonds: #status predicted  
F:37/Modified site: amidated carboxyl end (Ser) #status predicted

Query Match 10.2%; Score 40; DB 1; Length 37;

Best Local Similarity 28.1%; Pred. No. 1.4e+03;

Matches 9; Conservative 3; Mismatches 2; Indels 18; Gaps 2;

Qy 21 CDG---RCQRFCPNVVPKPLCIKICAPGVCVR 49

Db 18 CDGLYCSRSY-----PGCMCR 34

RESULT 18

NTSRPM

C:Species: Androctonus mauretanicus

C:Date: 15-Oct-1982 #sequence\_revision 15-Oct-1982 #text\_change 23-Aug-1996

C:Accession: A01758

Toxicon 23, 113-125, 1985

R:Rosso, J.P.; Rochat, H.

A:Title: Characterization of ten proteins from the venom of the Moroccan scorpion Androctonus mauretanicus

A:Reference number: A94318; MUID:85193276; PMID:3992595

A:Accession: A01758

A:Molecule type: protein

A:Residues: 1-35 <ROS>

C:Superfamily: scorpion neurotoxin

C:Keywords: neurotoxin; venom

F:1-18,4-25,15-30,19-32/Disulfide bonds: #status predicted

Query Match 10.1%; Score 39.5; DB 1; Length 35;

Best Local Similarity 31.4%; Pred. No. 1.5e+03;

Matches 11; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

Qy 7 GGRGKCPNSIFSRCDGRCQFCPNVVPKPLCIKI 41

Db 20 GGRGKCSRSY-----VGQCCLNRI 35

RESULT 19

S39034

Lipid transfer protein P1 - grape

C:Species: Vitis sp. (grape)

C:Date: 25-Dec-1994 #sequence\_revision 19-Apr-1996 #text\_change 17-Mar-1999

C:Accession: S39034

R:Coutos-Thievenot, P.; Jouenne, T.; Maes, O.; Guerbette, F.; Grosbois, M.; le Caer, J.P.

A:Title: Four 9-kDa proteins excreted by somatic embryos of grapevine are isoforms of lipid transfer protein

A:Reference number: S39034; MUID:94039144; PMID:8223644

A:Accession: S39034

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-38 <PGR>

C:Superfamily: phospholipid transfer protein

Query Match 10.1%; Score 39.5; DB 2; Length 38;

Best Local Similarity 55.6%; Pred. No. 1.6e+03;

Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 50 LGYLRNKKVKVCPRSKCG 67

Db 15 LGYLRNGGAV-PPGSSCG 31

RESULT 20

A34471

agitoxin 1 - scorpion (Leiurus quinquestriatus)

N:Alternate names: ACTX-1

C:Species: Leiurus quinquestriatus hebraeus

C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 23-May-1997

C:Accession: A54471

R:Garcia, M.L.; Garcia-Calvo, M.; Hidalgo, P.; Lee, A.; MacKinnon, R.

Biochemistry 33, 6834-6839, 1994

A:Title: Purification and characterization of three inhibitors of voltage-dependent K

A:Reference number: A54471; MUID:94263998; PMID:8204618

A:Accession: A54471

A:Molecule type: protein

A:Residues: 1-38 <GAR>

C:Superfamily: kalitoxin

C:Keywords: neurotoxin; potassium channel inhibitor; venom

F:8-28,14-33,18-35/Disulfide bonds: #status predicted

Query Match 10.0%; Score 39; DB 2; Length 38;

Best Local Similarity 27.3%; Pred. No. 1.8e+03;

Matches 12; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

Qy 20 RCDGRCQFCPNVVPKPLCIKICAPGVCVRLGYLRNKKVKVCP 63

Db 7 KCTG-----SPQCLKPKCKDAGM-RFGKINGKCHCTPK 38

RESULT 21

S43282

gallinacin - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

C:Accession: S43282

R:Harwig, S.S.L.; Swiderek, K.M.; Kokryakov, V.N.; Tan, L.; Lee, T.D.; Panyutich, E.A.

FEBS Lett. 342, 281-285, 1994

A:Title: Gallinacins: cysteine-rich antimicrobial peptides of chicken leukocytes.

A:Reference number: S43282; MUID:94200386; PMID:8150085

A:Accession: S43282

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-39 <HAR>

Query Match 10.0%; Score 39; DB 2; Length 39;

Best Local Similarity 36.7%; Pred. No. 1.9e+03;

Matches 11; Conservative 2; Mismatches 7; Indels 10; Gaps 2;

Qy 11 KCPSEIFSRCDGRCQFCPNVVPKPLCIK 40

Db 17 KCPYLTLS---GKCSRF-----HLCK 36

RESULT 22

B34923

omega-agatoxin IB - funnel-weaving spider (Agelenopsis aperta) (fragment)

C:Species: Agelenopsis aperta

C:Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 30-Sep-1993

C:Accession: B34923

R:Adams, M.E.; Bindokas, V.P.; Hasegawa, L.; Venema, V.J.

J. Biol. Chem. 265, 861-867, 1990

A:Title: Omega-Agatoxins: novel calcium channel antagonists of two subtypes from funnel-weaving spider (Agelenopsis aperta)

A:Reference number: A34923; MUID:90110147; PMID:2295621

A:Accession: B34923

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-36 <ADA>

Query Match 9.8%; Score 38.5; DB 2; Length 36;

Best Local Similarity 34.5%; Pred. No. 2e+03;

Matches 10; Conservative 4; Mismatches 10; Indels 5; Gaps 2;

Qy 5 GLGGRGKCPNSIFSRCDG---RCQRFCP 30

Db 3 GLPEGAECDDGNSCKCAGAWIKCR--CP 29

RESULT 23



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 27, 2003, 09:03:04 ; Search time 13 Seconds  
(without alignments)  
213.763 Million cell updates/sec

Title: US-09-506-978-1  
Perfect score: 391  
Sequence: 1 GGGGLGGRGKCPNSIFSR.....CRLGLRNKKKVCVPSKCG 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1266

Minimum DB seq length: 32  
Maximum DB seq length: 45

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.5	12.9	43	1 MTA_COLVI	P27086 colinus vir
2	50	12.8	38	1 SKL1 ANDMA	P24662 androctonus
3	48	12.3	40	1 BD01_BOVIN	P46168 bos taurus
4	47	12.0	38	1 SCA3_LEIQH	P46112 leiurus qui
5	46.5	11.9	38	1 SCA2_LEIQH	P27087 colinus vir
6	46.5	11.9	43	1 MTB_COLVI	P56686 androctonus
7	46	11.8	37	1 DEF4_ANDAU	P80389 gallus gall
8	45	11.5	39	1 AMPL_CHICK	P81502 aedes aegypt
9	45	11.5	40	1 DEF8_AEDAE	Q01157 lycopersico
10	45	11.5	43	1 GRW1_LICES	P82226 hadronyche
11	44	11.3	38	1 DEF4_LEIQH	P41965 leiurus qui
12	42.5	10.9	36	1 TXJB_HADVE	P82227 hadronyche
13	42	10.7	32	1 ITR4_CUCMA	P07853 cucurbita m
14	42	10.7	34	1 ITR2_MOMCO	P82409 momordica c
15	41.5	10.6	43	1 MT2_DROME	P11956 drosophila
16	40.5	10.4	34	1 ITR1_MOMCO	P82408 momordica c
17	40.5	10.4	38	1 DEF1_MITGA	P80571 mytilus gal
18	40	10.2	37	1 TXM2_AGEAP	P11058 agelenopsis
19	39.5	10.1	35	1 SCXP_ANDMA	P01498 androctonus
20	39.5	10.1	36	1 TXJA_HADVE	P82227 hadronyche
21	39.5	10.1	38	1 NLT1_VITXS	P80275 vitis sp. (
22	39.5	10.1	38	1 NLT2_VITXS	P33556 vitis sp. (
23	39	10.0	38	1 SCAL_LEIQH	P46110 leiurus qui
24	39	10.0	39	1 GLI2_CHICK	P46157 gallus gall
25	38.5	9.8	34	1 PTU1_PEITU	P58606 peirates tu
26	38.5	9.8	35	1 TXKS_STOHE	P29187 stoichiactis
27	38.5	9.8	36	1 TX1B_AGEAP	P15970 agelenopsis
28	38.5	9.8	37	1 TXJC_HADVE	P82228 hadronyche
29	38	9.7	42	1 MYX1_CROVV	P01476 crotalus vi
30	38	9.7	40	1 HEVP_HEVBR	P80359 hevea bras
31	38	9.7	45	1 TXO2_HADVE	P82852 hadronyche
32	37.5	9.6	35	1 SCXB_PANIM	P55928 pandinus im
33	37.5	9.6	37	1 RL36_MYCLE	Q9X7A2 mycobacteri

34 37 9.5 32 1 ITR2\_CUCSA  
35 37 9.5 32 1 ITR3\_CUCPE  
36 37 9.5 40 1 BD02\_BOVIN  
37 37 9.5 42 1 CXS3\_CONGE  
38 37 9.5 43 1 DEFA\_ZOPAT  
39 36.5 9.3 37 1 RL36\_BACSU  
40 36.5 9.3 37 1 RL36\_MYCTU  
41 36.5 9.3 38 1 SCX8\_LEIQH  
42 36.5 9.3 40 1 MT1\_DROME  
43 36.5 9.3 40 1 MT1\_DROSI  
44 36 9.2 33 1 Y656\_TREPA  
45 36 9.2 37 1 TXM4\_AGEAP  
46 36 9.2 37 1 TXM5\_AGEAP  
47 36 9.2 38 1 BD01\_BOVIN  
48 36 9.2 40 1 BD07\_BOVIN  
49 36 9.2 42 1 MYXC\_CRODU  
50 35.5 9.1 38 1 DEFI\_AESCY

## ALIGNMENTS

RESULT 1

MTA\_COLVI STANDARD; PRT; 43 AA.  
AC P27086;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Metallothionein A (MTA) (Fragment).  
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Odontophoridae; Colinus.  
OX NCBI\_Taxid=9014;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Liver;  
RC MEDLINE=93247066; PubMed=8483164;  
RA Shartzer K.L., Kage K., Sobieski R.J., Andrews G.K.;  
RT "Evolution of avian metallothionein: DNA sequence analyses of the  
turkey metallothionein gene and metallothionein cDNAs from pheasant  
J. Mol. Evol. 36:255-262(1993)."  
RL J. Mol. Evol. 36:255-262(1993).  
CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE  
RESIDUES THAT BIND VARIOUS HEAVY METALS.  
CC -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:  
FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA  
DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11  
CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE  
BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.  
CC -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.  
CC  
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CC  
CC EMBL; X62511; CAA44370.1; -  
DR PIR; S18173; S18173.  
DR PIR; S33378; S33378.  
DR PIR; S33380; S33380.  
DR PIR; S33382; S33382.  
DR HSP; P28184; LJI9.  
DR InterPro; IPR003019; Metallothion.  
DR InterPro; IPR000006; Metallothion\_vert.  
DR Pfam; PF00131; metalthio; 1.  
DR PROSITE; PS00203; METALLOTHIONEIN\_VRT; PARTIAL.  
KW Metal-binding; Metal-thiolate cluster.  
FT NON\_TER 1

34



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RESULT 4
SCA3_LEIQH          STANDARD;          PRT;          38 AA.
ID  SCA3_LEIQH
AC  P46112;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Agitoxin 3 (AGTX-3).
OS  Leiurus quinquestriatus hebraeus (Scorpion).
OC  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC  Buthoidea; Buthidae; Leiurus.
OX  NCBI_TaxID=6884;
RN  [1]
RP  SEQUENCE.
RX  TISSUE=Venom;
RX  MEDLINE=94263998; PubMed=8204618;
RA  Garcia M.L., Garcia-Calvo M., Hidalgo P., Lee A., Mackinnon R.;
RT  "Purification and characterization of three inhibitors of voltage-
RT  dependent K+ channels from Leiurus quinquestriatus var. hebraeus
RT  venom.";
RL  Biochemistry 33:6834-6839(1994).
CC  -!- FUNCTION: POTENT INHIBITOR OF SHAKER POTASSIUM CHANNELS AS WELL AS
CC  THE MAMMALIAN HOMOLOGS OF SHAKER.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC  CHANNEL INHIBITORS SUBFAMILY.
DR  HSSP; P46111; IAGT.
DR  InterPro: IPR001947; Scorpion_toxins.
DR  Pfam: PF00451; toxin_2; 1.
DR  ProDom: PD003586; Scorpion_toxins; 1.
DR  Neurotoxin; Scorp SHORT_TOXIN; 1.
KW  DISULFID 8 28 BY SIMILARITY.
FT  DISULFID 14 33 BY SIMILARITY.
FT  DISULFID 18 35 BY SIMILARITY.
FT  SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+)
FT  CHANNELS (POTENTIAL).
SQ  SEQUENCE 38 AA; 4107 MW; E5945513F87B51CE CRC64;

Query Match          12.0%; Score 47; DB 1; Length 38;
Best Local Similarity 37.8%; Pred. No. 68;
Matches 14; Conservative 3; Mismatches 16; Indels 4; Gaps 2;

Qy  30 PNVPV---PLCICKICAPGCVRLGKLNKKVCVPR 63
Db  3 PINVPTGSPQCKPKCKDAGM-RFGKCMNRKCHCTPK 38

RESULT 5
SCA2_LEIQH          STANDARD;          PRT;          38 AA.
ID  SCA2_LEIQH
AC  P46111;
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Agitoxin 2 (AGTX-2).
OS  Leiurus quinquestriatus hebraeus (Scorpion).
OC  Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC  Buthoidea; Buthidae; Leiurus.
OX  NCBI_TaxID=6884;
RN  [1]
RP  SEQUENCE.
RX  TISSUE=Venom;
RX  MEDLINE=94263998; PubMed=8204618;
RA  Garcia M.L., Garcia-Calvo M., Hidalgo P., Lee A., Mackinnon R.;
RT  "Purification and characterization of three inhibitors of voltage-
RT  dependent K+ channels from Leiurus quinquestriatus var. hebraeus
RT  venom.";
RL  Biochemistry 33:6834-6839(1994).
RN  [2]
RP  STRUCTURE BY NMR.

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RX  MEDLINE=96060078; PubMed=8520473;
RA  Krezel A.M., Kasibhatla C., Hidalgo P., Mackinnon R., Wagner G.;
RT  "Solution structure of the potassium channel inhibitor agitoxin 2:
RT  caliper for probing channel geometry.";
RL  Protein Sci. 4:1478-1489(1995).
CC  -!- FUNCTION: POTENT INHIBITOR OF SHAKER POTASSIUM CHANNELS AS WELL AS
CC  THE MAMMALIAN HOMOLOGS OF SHAKER.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC  CHANNEL INHIBITORS SUBFAMILY.
DR  PDB; IAGT; 10-JUL-95.
DR  InterPro: IPR001947; Scorpion_toxins.
DR  Pfam: PF00451; toxin_2; 1.
DR  ProDom: PD003586; Scorpion_toxins; 1.
DR  Neurotoxin; Scorp SHORT_TOXIN; 1.
KW  DISULFID 8 28 BY SIMILARITY.
FT  DISULFID 14 33 BY SIMILARITY.
FT  DISULFID 18 35 BY SIMILARITY.
FT  SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+)
FT  CHANNELS (POTENTIAL).
SQ  SEQUENCE 38 AA; 4097 MW; C8BB8513F87B51CD CRC64;

Query Match          11.9%; Score 46.5; DB 1; Length 38;
Best Local Similarity 39.3%; Pred. No. 77;
Matches 11; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

Qy  36 PLCICKICAPGCVRLGKLNKKVCVPR 63
Db  12 PQCKPKCKDAGM-RFGKCMNRKCHCTPK 38

RESULT 6
MTB_COLVI
ID  MTB_COLVI          STANDARD;          PRT;          43 AA.
AC  P27087;
DT  01-AUG-1992 (Rel. 23, Created)
DT  01-AUG-1992 (Rel. 23, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Metallothionein B (MTB) (Fragment).
OS  Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC  Odontophorinae; Colinus.
OX  NCBI_TaxID=9014;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Liver;
RX  MEDLINE=93247066; PubMed=8483164;
RA  Shartzer K.L., Kage K., Sobleski R.J., Andrews G.K.;
RT  "Evolution of avian metallothionein: DNA sequence analyses of the
RT  turkey metallothionein gene and metallothionein cDNAs from pheasant
RT  and quail.";
RL  J. Mol. Evol. 36:255-262(1993).
CC  -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC  RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC  -!- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC  FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC  DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC  CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC  BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC  -!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  -----
DR  EMBL; X62512; CAA44371.1; -.
DR  PIR; S18174; S18174.

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Thu Feb 27 09:12:57 2003

PIR: S33379; S33379.  
 HSP: P04355; 1MRT.  
 DR InterPro: IPR003019; Metallthion..  
 DR InterPro: IPR000006; Metallthion.vert.  
 DR Pfam: PF00131; metalthio; 1.  
 DR PROSITE: PS00203; METALLOTHIONEIN\_VRT; PARTIAL.  
 KW Metal-binding; Metal-thiolate cluster.  
 FT NON\_TER 1 1  
 FT DOMAIN <1 15 BETA.  
 FT DOMAIN 17 >43 ALPHA.  
 FT METAL 2 2 CLUSTER B.  
 FT METAL 6 6 CLUSTER B.  
 FT METAL 8 8 CLUSTER B.  
 FT METAL 11 11 CLUSTER B.  
 FT METAL 13 13 CLUSTER B.  
 FT METAL 16 16 CLUSTER B.  
 FT METAL 20 20 CLUSTER A.  
 FT METAL 21 21 CLUSTER A.  
 FT METAL 23 23 CLUSTER A.  
 FT METAL 24 24 CLUSTER A.  
 FT METAL 28 28 CLUSTER A.  
 FT METAL 31 31 CLUSTER A.  
 FT METAL 35 35 CLUSTER A.  
 FT METAL 37 37 CLUSTER A.  
 FT NON\_TER 43 43  
 SQ SEQUENCE 43 AA: 4429 MW; 1612EB40EE6EB875 CRC64;  
 Query Match 11.9%; Score 46.5; DB 1; Length 43;  
 Best Local Similarity 31.0%; Pred. No. 84;  
 Matches 13; Conservative 5; Mismatches 17; Indels 7; Gaps 3;  
 QY 8 GRGKCPSEIFSRDGRCPNVPKPLKICAPCCVCR 49  
 DB 4 GSKCKN-----CRKRS-CRKSCCCCPAG--CNCVKGCVC 38  
 RESULT 7  
 DEF4\_ANDAU  
 ID DEF4\_ANDAU STANDARD; PRT; 37 AA.  
 AC P56686; P81618;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE 4 kDa defensin.  
 OS Androctonus australis hector (Sahara scorpion).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
 OC Butyridae; Buthidae; Androctonus.  
 OX NCBI\_TaxID=70175;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=97094646; PubMed=8939880;  
 RA Ehret-Sabatier L., Loew D., Goyffon M., Fehlbaum P., Hoffmann J.A.,  
 RA van Dorselaer A., Bulet P.;  
 RT "Characterization of novel cysteine-rich antimicrobial peptides from  
 scorpion blood";  
 RL J. Biol. Chem. 271:29537-29544 (1996).  
 CC -1- FUNCTION: ACTIVE AGAINST GRAM-POSITIVE BACTERIA.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray.  
 CC -1- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.  
 DR HSP: P10891; IICA.  
 DR InterPro: IPR001542; Defensin\_anpod.  
 DR Pfam: PF01097; Arthro\_defensin; 1.  
 DR PROSITE: PS00425; ARTHROPOD\_DEFENSINS; 1.  
 KW Antibiotoxic.  
 FT DISULFID 4 25 BY SIMILARITY.  
 FT DISULFID 11 33 BY SIMILARITY.  
 FT DISULFID 15 35 BY SIMILARITY.  
 SQ SEQUENCE 37 AA: 4212 MW; AB1363ECE3FB84C1 CRC64;  
 Query Match 11.8%; Score 46; DB 1; Length 37;  
 Best Local Similarity 27.1%; Pred. No. 85;

Matches 13; Conservative 5; Mismatches 16; Indels 14; Gaps 3;  
 QY 2 GFGLGGRGKCPSEIFSRDGRCPNVPK-PLCIKICAPGCVC 48  
 DB 1 GFG-----CPFNQ-----GACHRHCHSIRRRGGYAGLKFQKQTC 35  
 RESULT 8  
 AMPL1\_CHICK  
 ID AMPL1\_CHICK STANDARD; PRT; 39 AA.  
 AC P80389;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Antimicrobial peptide, CHP1 (Chicken heterophil peptide 1).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP MEDLINE=95053386; PubMed=7964174;  
 RX Evans E.W., Beach G.G., Wunderlich J., Harmon B.G.;  
 RT "Isolation of antimicrobial peptides from avian heterophils";  
 RL J. Leukoc. Biol. 56:661-665 (1994).  
 CC -1- FUNCTION: BACTERICIDAL ACTIVITY; INHIBITS STAPHYLOCOCCUS AUREUS  
 CC AND ESCHERICHIA COLI.  
 KW Antibiotic.  
 FT DISULFID 6 28 BY SIMILARITY.  
 FT DISULFID 13 34 BY SIMILARITY.  
 FT DISULFID 18 35 BY SIMILARITY.  
 SQ SEQUENCE 39 AA: 4480 MW; 5DDF1051693D254E CRC64;  
 Query Match 11.5%; Score 45; DB 1; Length 39;  
 Best Local Similarity 40.0%; Pred. No. 11e+02;  
 Matches 12; Conservative 2; Mismatches 6; Indels 10; Gaps 2;  
 QY 11 KCPSNEIFSRDGRCPNVPKPLKIC 40  
 DB 17 KCPSLTLLS---GKCSRFV-----LOCK 36  
 RESULT 9  
 DEF4\_AEDAE  
 ID DEF4\_AEDAE STANDARD; PRT; 40 AA.  
 AC P81602;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Defensin B.  
 OS Aedes aegypti (Yellowfever mosquito).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;  
 OC Culicoidae; Aedes.  
 OX NCBI\_TaxID=7159;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Liverpool;  
 RX MEDLINE=95360030; PubMed=7633471;  
 RA Lowenberger C., Bulet P., Charlet M., Hetru C., Hodgeman B.,  
 RA Christensen B.M., Hoffmann J.A.;  
 RT "Insect immunity: isolation of three novel inducible antibacterial  
 defensins from the vector mosquito, Aedes aegypti";  
 RL Insect Biochem. Mol. Biol. 25:867-873 (1995).  
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE MOSTLY AGAINST GRAM-POSITIVE  
 CC BACTERIA.  
 CC -1- INDUCTION: By bacterial infection.  
 CC -1- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.  
 DR HSP: P10891; IICA.  
 DR InterPro: IPR001542; Defensin\_anpod.  
 DR InterPro: IPR003614; Knot1.  
 DR Pfam: PF01097; Arthro\_defensin; 1.

AC	P41965;
DT	01-NOV-1995 (Rel. 32, Created)
DT	01-NOV-1995 (Rel. 32, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	4 kDa defensin (Antibacterial 4 kDa peptide).
OS	Leiurus quinquestriatus hebraeus (Scorpion).
DE	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC	Buthoidea; Buthidae; Leiurus.
OX	NCBI_TaxID=6884;
RN	[1]
RP	SEQUENCE.
RP	TISSUE=Hemolymph;
RC	MEDLINE=93326112; PubMed=8333834;
RX	Coclanich S., Goffon M., Bontems F., Bouet P., Menez A.,
RA	Hoffmann J.A.;
RT	"Purification and characterization of a scorpion defensin, a 4kDa
RT	antibacterial peptide presenting structural similarities with insect
RT	defensins and scorpion toxins.";
RL	Biochem. Biophys. Res. Commun. 194:17-22(1993).
CC	-!- FUNCTION: ANTIBACTERIAL PROTEIN AGAINST GRAM-POSITIVE BACTERIA;
CC	MAY ACT VIA MEMBRANE-PERMEABILIZATION OF THESE CELLS.
CC	-!- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.
CC	PIR; JN0613; JN0613.
DR	HSP; P10891; IICA.
DR	InterPro: IPR001542; Defensin_apod.
DR	Pfam: PF01097; Arthro.defensin; 1.
DR	PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
KW	Antibiotic.
FT	DISULFID 4 25 BY SIMILARITY.
FT	DISULFID 11 33 BY SIMILARITY.
FT	DISULFID 15 35 BY SIMILARITY.
SQ	SEQUENCE 38 AA; 4326 MW; DF35FB21ECE3FB84 CRC64;
QY	Query Match 11.3%; Score 44; DB 1; Length 38;
DB	Best Local Similarity 27.1%; Pred. No. 1.4e+02;
	Matches 13; Conservative 4; Mismatches 17; Indels 14; Gaps
	2 GFGGLGRGKGPSNEITSRCDCQRFCPNVPK-PLCIKICAPGCVC 48 ;
	1 GFG-----CPLNQ-----GACHRHCRIRRRGGYCAGFFKQTCTC 35
	:
RESULT 12	
ID	TXJB_HADVE STANDARD; PRT; 36 AA.
IC	P82226;
DD	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Janus-atracotoxin-HvIb (J-AcTx-HvIb).
OS	Hadronyche versuta (Blue mountains funnel-web spider) (Atrax
OS	versutus).
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC	Mygalomorphae; Hexatheilidae; Hadronychae.
NR	NCBI_TaxID=6904;
RN	[1]
RP	SEQUENCE.
RP	TISSUE=Venom;
RC	MEDLINE=20343014; PubMed=10881200;
RX	Wang X.-H., Connor M., Maciejewski M.W., Howden M.E.H.,
RA	Nicholson G.M., Christie M.J., King G.F.;
RT	"Discovery and characterization of a family of insecticidal
RT	neurotoxins with a rare vicinal disulfide bridge.";
RL	Nat. Struct. Biol. 7:505-513(2000).
CC	-!- FUNCTION: INSECTICIDAL NEUROTOXIN.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Expressed by the venom gland.
DR	HSP; P82228; IDL0.
DR	Toxin; Neurotoxin.
KW	DISULFID 3 17 BY SIMILARITY.
FT	DISULFID 10 22 BY SIMILARITY.
FT	DISULFID 13 14 BY SIMILARITY.
FT	DISULFID 16 33 BY SIMILARITY.

SQ SEQUENCE 36 AA: 3651 MW; D23A442560B89997 CRC64;  
Query Match 10.9%; Score 42.5; DB 1; Length 36;  
Best Local Similarity 26.7%; Pred. No. 1.9e+02;  
Matches 12; Conservative 3; Mismatches 13; Indels 17; Gaps 2;

QY 17 IFSRCDGRCRQFNVVVKPLCKIKCAPGCVCR-----LGYLRN 55  
DB 2 ICTGADRPCAACCP-----CCGCTSCQGPENGVSYCRN 35

RESULT 13  
ID ITRA\_CUCMA STANDARD; PRT; 32 AA.  
AC P07853;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 01-MAY-1992 (Rel. 22, Last annotation update)  
DE Trypsin inhibitors IV and III (CMTI-IV and CMTI-III).  
OS Cucurbita maxima (Pumpkin) (Winter squash).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.  
OX NCBI\_TaxID=3661;  
RN [1]  
RP SEQUENCE (CMT-IV).  
RC TISSUE=Seed;  
RX MEDLINE=85149300; PubMed=3977882;  
RA Wleczorek M., Otlewski J., Cook J., Parks K., Leluk J.,  
RA Wleczorek M., Otlewski J., Polanowski A., Wilusz T., Laskowski M. Jr.;  
RT "The squash family of serine proteinase inhibitors. Amino acid  
RT sequences and association equilibrium constants of inhibitors from  
RT squash, summer squash, zucchini, and cucumber seeds.";  
RL Biochem. Biophys. Res. Commun. 126:646-652(1985).  
RN [2]  
RP SEQUENCE (CMT-III).  
RC TISSUE=Seed;  
RX MEDLINE=83184077; PubMed=6840699;  
RA Wilusz T., Wleczorek M., Polanowski A., Denton A., Cook J.,  
RA Laskowski M. Jr.;  
RT "Amino-acid sequence of two trypsin isoinhibitors, ITD I and ITD III  
RT from squash seeds (Cucurbita maxima).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:93-95(1983).  
RN [3]  
RP PRELIMINARY SEQUENCE (CMT-III).  
RC TISSUE=Seed;  
RX MEDLINE=82005824; PubMed=7275008;  
RA Nowak K., Slominska A., Polanowski A., Wleczorek M., Wilusz T.;  
RT "Trypsin inhibitor III from squash seeds (Cucurbita maxima), its  
RT reactive site and proposed amino acid sequence.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 362:1017-1019(1981).  
RN [4]  
RP STRUCTURE BY NMR OF CMT-III.  
RX MEDLINE=92118901; PubMed=1731946;  
RA Krishnamoorthi R., Gong Y., Lin C.-L.S., Vandervelde D.;  
RT "Two-dimensional NMR studies of squash family inhibitors. Sequence-  
RT specific proton assignments and secondary structure of reactive-site  
RT hydrolyzed Cucurbita maxima trypsin inhibitor III.";  
RL Biochemistry 31:898-904(1992).  
RN [5]  
RP -I- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE  
INHIBITORS.  
CC PIR; A01313; TIPU3.  
DR PIR; S07156; S07156.  
DR HSSP; P01074; ICTI.  
DR InterPro; IPR000737; Squash.  
DR Pfam; PF00299; squash; 1.  
DR PRINTS; PR00293; SQUASHINHTR.  
DR ProDom; PD003401; Squash; 1.  
DR SMART; SM00286; PTI; 1.  
DR PROSITE; PS00286; SQUASH\_INHIBITOR; 1.  
CC KRISNAMOOORTHIL R., GONG Y., LIN C.-L.S., VANDERVELDE D.;  
RT "Two-dimensional NMR studies of squash family inhibitors. Sequence-  
RT specific proton assignments and secondary structure of reactive-site  
RT hydrolyzed Cucurbita maxima trypsin inhibitor III.";  
RL Biochemistry 31:898-904(1992).  
RN [6]  
RP -I- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE  
INHIBITORS.  
CC PIR; A01313; TIPU3.  
DR PIR; S07156; S07156.  
DR HSSP; P01074; ICTI.  
DR InterPro; IPR000737; Squash.  
DR Pfam; PF00299; squash; 1.  
DR PRINTS; PR00293; SQUASHINHTR.  
DR ProDom; PD003401; Squash; 1.  
DR SMART; SM00286; PTI; 1.  
DR PROSITE; PS00286; SQUASH\_INHIBITOR; 1.  
KW Serine protease inhibitor.  
FT CHAIN 1 32 CMTI-IV.  
FT CHAIN 4 32 CMTI-III.

FT ACT\_SITE .8 9 REACTIVE BOND.  
FT DISULFID 6 23 BY SIMILARITY.  
FT DISULFID 13 25 BY SIMILARITY.  
FT DISULFID 19 31 BY SIMILARITY.  
SQ SEQUENCE 32 AA: 3669 MW; 0F591120B0137512 CRC64;  
Query Match 10.7%; Score 42; DB 1; Length 32;  
Best Local Similarity 34.8%; Pred. No. 2e+02;  
Matches 8; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 26 QRECPNVVVKPLCKIKCAPGCV 48  
DB 3 ERVCPRLMKCKKDSCLAEVC 25

RESULT 14  
ID ITR2\_MOMCO STANDARD; PRT; 34 AA.  
AC P82409;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Trypsin inhibitor II (MCOTI-II).  
OS Momordica cochinchinensis (Spiny bitter cucumber).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.  
OX NCBI\_TaxID=3674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Seed;  
RX MEDLINE=20263490; PubMed=10801322;  
RA Hernandez J.-F., Gagnon J., Chiche L., Nguyen T.M., Andrieu J.-P.,  
RA Heitz A., Trinh T., Pham T.T.C., Le Nguyen D.;  
RT "Squash trypsin inhibitors from Momordica cochinchinensis exhibit an  
RT atypical macrocyclic structure.";  
RL Biochemistry 39:5722-5730(2000).  
RN [2]  
RP -I- FUNCTION: INHIBITS TRYPSIN; PROBABLY PARTICIPATES IN A PLANT  
DEFENSE MECHANISM.  
CC -I- PTM: A CYCLIC SUCCINIMIDE MAY BE FORMED BETWEEN ASP-4 AND GLY-5  
CC RESIDUES WHICH CAN BE TRANSFORMED TO A BETA-ASPARTYL BOND. SO  
CC THERE EXISTS THREE ISOFORMS OF MCOTI-II, NORMAL, WITH SUCCINIMIDE  
CC OR WITH A BETA-ASPARTYL BOND.  
CC -I- PTM: THIS IS A CYCLIC PEPTIDE.  
CC -I- MASS SPECTROMETRY: MW=3453; MW ERR=0.2; METHOD=Electrospray.  
CC -I- SIMILARITY: BELONGS TO THE SQUASH FAMILY OF SERINE PROTEASE  
INHIBITORS.  
CC HSSP; P01074; IBOXJ.  
DR InterPro; IPR000737; Squash.  
DR Pfam; PF00299; squash; 1.  
DR PRINTS; PR00293; SQUASHINHTR.  
DR ProDom; PD003401; Squash; 1.  
DR SMART; SM00286; PTI; 1.  
DR PROSITE; PS00286; SQUASH\_INHIBITOR; 1.  
KW Serine protease inhibitor.  
FT ACT\_SITE 10 11 REACTIVE BOND.  
FT DISULFID 8 25 BY SIMILARITY.  
FT DISULFID 15 27 BY SIMILARITY.  
FT DISULFID 21 33 BY SIMILARITY.  
SQ SEQUENCE 34 AA: 3477 MW; 8F7D0B4C048BB93A CRC64;  
Query Match 10.7%; Score 42; DB 1; Length 34;  
Best Local Similarity 33.3%; Pred. No. 2.1e+02;  
Matches 7; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 29 CPNVVVKPLCKIKCAPGCVCR 49  
DB 8 CPKILKCRDSDCPGACICR 28

RESULT 15  
ID MT2\_DRONE STANDARD; PRT; 43 AA.  
FT ACT\_SITE .8 9 REACTIVE BOND.  
FT DISULFID 6 23 BY SIMILARITY.  
FT DISULFID 13 25 BY SIMILARITY.  
FT DISULFID 19 31 BY SIMILARITY.  
SQ SEQUENCE 32 AA: 3669 MW; 0F591120B0137512 CRC64;  
Query Match 10.7%; Score 42; DB 1; Length 32;  
Best Local Similarity 34.8%; Pred. No. 2e+02;  
Matches 8; Conservative 3; Mismatches 12; Indels 0; Gaps 0;



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KW Serine protease inhibitor.
FT ACT_SITE 10 11 REACTIVE BOND.
FT DISULFID 8 25 BY SIMILARITY.
FT DISULFID 15 27 BY SIMILARITY.
FT DISULFID 21 33 BY SIMILARITY.
SQ SEQUENCE 34 AA; 3505 MW; 8F7D0B4C162C935A CRC64;

Query Match 10.4%; Score 40.5; DB 1; Length 34;
Best Local Similarity 30.0%; Pred. No. 3e+02;
Matches 12; Conservative 2; Mismatches 9; Indels 17; Gaps 3;

QY 10 GKCPNEIFSRCDGRCQFCPNVVPKPLCIKICAPGCVCVCR 49
    ||| :||| ||| |||
    6 GVCP--KILQRC--RRSDCPG-----ACICR 28

Db

RESULT 17
DEFL_MYTGA
ID DEFL_MYTGA STANDARD; PRT; 38 AA.
AC P80571;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Defensin MGD-1.
GN FH3.
OS Mytilus galloprovincialis (Mediterranean mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=29158;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=97025339; PubMed=8925841;
RA Hubert F., Noel T., Roch P.;
RT "A member of the arthropod defensin family from edible Mediterranean
RT mussels (Mytilus galloprovincialis).";
RL Eur. J. Biochem. 240:302-306(1996).
RN [2]
RP ERRATUM.
RA Hubert F., Noel T., Roch P.;
RL Eur. J. Biochem. 240:815-815(1996).
CC -!- SIMILARITY: BELONGS TO THE ARTHROPOD DEFENSIN FAMILY.
DR InterPro: IPR001542; Defensin_arpod.
DR Pfam: PF01097; Arthro_defensin; 1.
DR PROSITE: PS00425; ARTHROPOD_DEFENSINS; 1.
KW Antibiotic.
FT DISULFID 4 25 BY SIMILARITY.
FT DISULFID 10 33 BY SIMILARITY.
FT DISULFID 14 35 BY SIMILARITY.
FT DISULFID 21 38 BY SIMILARITY.
SQ SEQUENCE 38 AA; 4275 MW; 6F1C0CDCF0E69E76 CRC64;

Query Match 10.4%; Score 40.5; DB 1; Length 38;
Best Local Similarity 34.4%; Pred. No. 3e+02;
Matches 11; Conservative 3; Mismatches 7; Indels 11; Gaps 3;

QY 2 GFGLGGRGKCPN-EIFSRC---DGRQRCFC 29
    ||| ||| : ||| : ||| :
    1 GFG-----CPNNYQCHRHCKSIPIRGCGGYC 25

Db

RESULT 18
TXM2_AGEAP
ID TXM2_AGEAP STANDARD; PRT; 37 AA.
AC P11058;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mu-agenotoxin 2.
OS Agelenopsis aperta (Funnel-web spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Agelenidae; Agelenopsis.
OX NCBI_TaxID=6908;

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RN SEQUENCE.
RP MEDLINE=89123282; PubMed=2914898;
RX Skinner W.S., Adams M.E., Quistad G.B., Kataoka H., Cesarin B.J.,
RA Enderlin F.E., Schooley D.A.;
RT "Purification and characterization of two classes of neurotoxins from
RT the funnel web spider, Agelenopsis aperta.";
RL J. Biol. Chem. 264:2150-2155(1989).
CC -!- FUNCTION: CAUSE IRREVERSIBLE PARALYSIS IN LEPIDOPTEROUS INSECTS
CC BY MASSIVE TRANSMITTER RELEASE (WHICH IS MEDIATED BY GLUTAMIC ACID
CC RECEPTORS) FROM PRESYNAPTIC STORES AT NEUROMUSCULAR JUNCTIONS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: BELONGS TO THE MU-AGATOXIN FAMILY.
DR PIR: B32038; B32038.
DR HSSP: P11060; 1E1U.
DR Toxin; Neurotoxin.
KW DISULFID 2 18 BY SIMILARITY.
FT DISULFID 9 23 BY SIMILARITY.
FT DISULFID 17 33 BY SIMILARITY.
FT DISULFID 25 31 BY SIMILARITY.
SQ SEQUENCE 37 AA; 4110 MW; 8900D367B4F096CD CRC64;

Query Match 10.2%; Score 40; DB 1; Length 37;
Best Local Similarity 28.1%; Pred. No. 3.7e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 18; Gaps 2;

QY 21 CDG---RCQRCFPCPNVVPKPLCIKICAPGCVCVCR 49
    ||| ||| : ||| : ||| :
    18 CDGLYCSCRSY-----PGCMCR 34

Db

RESULT 19
SCXP_ANDMA
ID SCXP_ANDMA STANDARD; PRT; 35 AA.
AC P01498;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotoxin P2.
OS Androctonus mauretanicus mauretanicus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthoidea; Buthidae; Androctonus.
OX NCBI_TaxID=6860;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85193276; PubMed=3992595;
RA Rosso J.P., Rochat H.;
RT "Characterization of ten proteins from the venom of the Moroccan
RT scorpion Androctonus mauretanicus mauretanicus, six of which are
RT toxic to the mouse.";
RL Toxicon 23:113-125(1985).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY.
DR PIR: A01758; NTSRPM.
DR HSSP: P15222; 1S1S.
KW Neurotoxin.
FT DISULFID 1 18 BY SIMILARITY.
FT DISULFID 4 25 BY SIMILARITY.
FT DISULFID 15 30 BY SIMILARITY.
FT DISULFID 19 32 BY SIMILARITY.
SQ SEQUENCE 35 AA; 3673 MW; 213B69262289EB5A CRC64;

Query Match 10.1%; Score 39.5; DB 1; Length 35;
Best Local Similarity 31.4%; Pred. No. 4e+02;
Matches 11; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

QY 7 GGRGKCPNNEIFSRCDGRCQFCPNVVPKPLCIKI 41
    ||||| ||| : ||| : ||| :
    20 GGRGK-----VGQCQLCNRI 35

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RESULT 21
INUTL_VITSX
NLTIID      STANDARD;      PRT;      38 AA.
P80275;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Nonspecific lipid-transfer protein P1 (LTP P1) (Fragment).
Vitis sp. (Grape).
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
Vitis.
NCBI_TaxID=3604;
[1]
SEQUENCE.
STRAIN=V. vinifera X Berlanchen cv. Rootstock 41B;
MEDLINE=94039144; PubMed=8223644;
Coutos-Thievenot P., Jouenne T., Maes O., Guerbet F., Grosbois M.,
le Caer J.-P., Boulay M., Deloire A., Kader J.-C., Guern J.;
"Four 9-kDa proteins excreted by somatic embryos of grapevine are
isoforms of lipid-transfer proteins.";
Eur. J. Biochem. 217:885-889(1993).
-!- FUNCTION: PLANT NONSPECIFIC LIPID-TRANSFER PROTEINS TRANSFER
PHOSPHOLIPIDS AS WELL AS GALACTOLIPIDS ACROSS MEMBRANES. MAY PLAY
A ROLE IN WAX OR CUTIN DEPOSITION IN THE CELL WALLS OF EXPANDING
EPIDERMAL CELLS AND CERTAIN SECRETORY TISSUES.
-!- SIMILARITY: BELONGS TO THE PLANT LTP FAMILY.
HSSP: P19656; 1M2M
InterPro: IPR000528; plant_LTP.
InterPro: IPR001768; Try/amyl_inhbr.
Pfam: PF00234; trypt_alpha_amyl; 1

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RC TISSUE=Venom;
RX MEDLINE=94263998; PubMed=8204618;
RA Garcia M.L., Garcia-Calvo M., Hidalgo P., Lee A., Mackinnon R.;
RT "Purification and characterization of three inhibitors of voltage-
RT dependent K+ channels from Laelurus quinquestriatus var. hebraeus
RT venom.";
RL Biochemistry 33:6834-6839(1994).
CC -!- FUNCTION: POTENT INHIBITOR OF SHAKER POTASSIUM CHANNELS AS WELL AS
CC THE MAMMALIAN HOMOLOGS OF SHAKER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CC CHANNEL INHIBITORS SUBFAMILY.
DR HSP; P46111; IACT.
DR InterPro; IPR001947; Scorpion_toxins.
DR Pfam; PF00451; toxin_2; 1.
DR ProDom; PD003586; Scorpion_toxins; 1.
DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
KW Neurotoxin; Potassium channel inhibitor.
FT DISULFID 8 28 BY SIMILARITY.
FT DISULFID 14 33 BY SIMILARITY.
FT DISULFID 18 35 BY SIMILARITY.
FT SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+)
FT CHANNELS (POTENTIAL).
FT SEQUENCE 38 AA; 4021 MW; A0951113F87B51CE CRC64;

Query Match 10.0%; Score 39; DB 1; Length 38;
Best Local Similarity 27.3%; Pred. No. 4.8e+02;
Matches 12; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

QY 20 RGRGRCRQPCPNVWPVKLCIKICAPGCVCRGLYLNKKKVCVPR 63
DB 7 KCTG-----SPOCLPKCKDAGM-RFGKCKNGKCHCTPK 38

RESULT 24
GLL2_CHICK
ID GLL2_CHICK STANDARD; PRT; 39 AA.
AC P46157;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Gallinacin 1 alpha.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RC STRAIN=Cross Broiler-6; TISSUE=Leukocyte;
RX MEDLINE=94200386; PubMed=8150085;
RA Harvig S.S.L., Swiderok K.M., Kokryakov V.N., Tan L., Lee T.D.,
RA Panyutich E.A., Aleshina G.M., Shamova O.V., Lehrer R.I.;
RT "Gallinacins: cysteine-rich antimicrobial peptides of chicken
RT leukocytes.";
RL FEBS Lett. 342:281-285(1994).
CC -!- FUNCTION: HAS BACTERICIDAL ACTIVITY. POTENT AGAINST E. COLI ML-35,
CC L. MONOCYTOGENES EGD AND C. ALBICANS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC GRANULES.
CC -!- SIMILARITY: BELONGS TO THE BETA-DEFENSIN FAMILY.
KW Antibiotic.
FT DISULFID 6 34 BY SIMILARITY.
FT DISULFID 13 28 BY SIMILARITY.
FT DISULFID 18 35 BY SIMILARITY.
FT SEQUENCE 39 AA; 4587 MW; AFAF105C0441F499 CRC64;

Query Match 10.0%; Score 39; DB 1; Length 39;
Best Local Similarity 36.7%; Pred. No. 4.9e+02;
Matches 11; Conservative 2; Mismatches 7; Indels 10; Gaps 2;

QY 11 KCPSNEIFSRGRCGRFCPCPNVWPVKPLCTK 40
DB 17 KCPYLTLIS--GKCSR-----HLCKK 36

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RESULT 25
PTUL_PTITU
ID PTUL_PTITU STANDARD; PRT; 34 AA.
AC P58606;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toxin Ptul.
OS Peirates turpis (Assassin bug).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
OC Heteroptera; Panheteroptera; Cimicomorpha; Reduviidae; Peiratiinae;
OC Peirates.
OX NCBI_TaxID=181095;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, SYNTHESIS, AND CHARACTERIZATION.
RC TISSUE=Saliva;
RX MEDLINE=21316029; PubMed=11423127;
RA Corzo G., Adachi-Akahane S., Nagao T., Kusui Y., Nakajima T.;
RT "Novel peptides from assassin bugs (Hemiptera: Reduviidae): isolation,
RT chemical and biological characterization.";
RL PEBS Lett. 499:256-261(2001).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=21526409; PubMed=11669615;
RA Bernard C., Corzo G., Mosbah A., Nakajima T., Darbon H.;
RT "Solution structure of Ptul, a toxin from the assassin bug Peirates
RT turpis that blocks the voltage-sensitive calcium channel N-type.";
RL Biochemistry 40:12795-12800(2001).
CC -!- FUNCTION: Binds reversibly and blocks N-type voltage-gated calcium
CC channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Produced by the venomous saliva.
CC -!- MASS SPECTROMETRY: MW=3615.1; METHOD=MALDI.
DR PDB; 1I26; 21-NOV-01.
KW Calcium channel inhibitor; Toxin; Neurotoxin; 3D-structure.
FT DISULFID 5 20
FT DISULFID 12 26
FT DISULFID 19 33
FT SEQUENCE 34 AA; 3621 MW; 6B58A20A9E6B6FFA CRC64;

Query Match 9.8%; Score 38.5; DB 1; Length 34;
Best Local Similarity 37.9%; Pred. No. 4.9e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 7; Gaps 2;

QY 38 CIKICAPGCVCRGLYLNKKKVCVPRSKC 66
DB 5 CI---APGAPC----FGTDRKPCPNRAWC 26

Search completed: February 27, 2003, 09:05:05
Job time : 15 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 27, 2003, 09:03:04 ; Search time 28 Seconds  
(without alignments)  
493.041 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGFGLGGRKCPSEIFSR.....CRLGLRNKKVCVPSKCG 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 13368

Minimum DB seq length: 32

Maximum DB seq length: 45

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL\_21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriophage.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	62.5	16.0	40	13	Q98TP9		Q98tp9 platichthys
2	62.5	16.0	44	11	Q99KF9		Q99kf9 mus musculus
3	53	13.6	39	13	Q9PVG7		Q9pv7 xiphophorus
4	48.5	12.4	41	4	Q9UDP7		Q9udp7 homo sapien
5	47.5	12.1	37	11	Q9QX87		Q9qx87 rattus norv
6	47	12.0	41	13	Q9PVG6		Q9pv6 xiphophorus
7	45	11.5	36	10	Q02023		Q02023 lycopersico
8	44.5	11.4	37	4	Q9H499		Q9h499 homo sapien
9	44	11.3	40	4	Q8WV73		Q8wv73 homo sapien
10	44	11.3	45	10	Q9LW92		Q9lw92 nicotiana t
11	42.5	10.9	42	5	Q18625		Q18625 schistosoma
12	42	10.7	39	5	P82380		P82380 stomoxys ca
13	41.5	10.6	43	5	Q9VDN2		Q9vdn2 drosophila
14	41.5	10.6	43	13	Q8UUG4		Q8uug4 gallus gall
15	41.5	10.6	45	10	O81529		O81529 mesembryant
16	40	10.2	33	5	Q17071		Q17071 antheraea p

17	40	10.2	37	5	P83259	P83259 paracoelote
18	40	10.2	45	5	Q9VM82	Q9vm82 drosophila
19	39	10.0	35	10	Q942I4	Q942i4 oryza sativ
20	39	10.0	42	16	Q8XTX4	Q8xtx4 trystonia s
21	38	9.7	38	10	Q8W2G7	Q8w2g7 oryza sativ
22	37.5	9.6	42	8	Q9MRL7	Q9mrl7 daucus caro
23	37	9.5	33	4	Q9UD12	Q9ud12 homo sapien
24	37	9.5	41	11	Q99PH5	Q99ph5 mus musculu
25	37	9.5	43	5	Q9W4K6	Q9w4k6 drosophila
26	36.5	9.3	32	4	Q8WTO0	Q8wtq0 homo sapien
27	36.5	9.3	33	4	Q9UIH2	Q9uih2 homo sapien
28	36.5	9.3	37	16	Q927N0	Q927n0 listeria mo
29	36.5	9.3	43	2	O05188	O05188 bacillus su
30	36	9.2	40	12	Q91K65	Q91k65 hepatitis c
31	36	9.2	42	10	O23471	O23471 arabidopsis
32	36	9.2	43	5	Q95P80	Q95p80 carcinus ma
33	35.5	9.1	32	6	Q77A93	Q77a93 lemur catta
34	35.5	9.1	38	4	Q9UGU2	Q9ugu2 homo sapien
35	35.5	9.1	39	5	Q9RX98	Q9tx98 caenorhabdi
36	35.5	9.1	40	12	O57150	O57150 human herpe
37	35.5	9.1	41	12	Q81248	Q81248 hepatitis c
38	35.5	9.1	41	12	O81252	O81252 hepatitis c
39	35.5	9.1	41	12	O81253	O81253 hepatitis c
40	35.5	9.1	42	3	Q9Y733	Q9y733 candida tro
41	35.5	9.1	42	3	Q9Y734	Q9y734 candida tro
42	35.5	9.1	43	10	Q9LQI3	Q9lqi3 arabidopsis
43	35.5	9.1	43	11	Q8R3Y9	Q8r3y9 mus musculu
44	35.5	9.1	43	12	Q8S597	Q8s597 reovirus sp
45	35	9.0	32	10	O8S527	O8s527 ipomoea bat
46	35	9.0	34	4	Q14253	Q14253 homo sapien
47	35	9.0	36	16	Q9KLR9	Q9klr9 vibrio chol
48	35	9.0	36	16	Q99QX1	Q99qx1 staphylococ
49	35	9.0	40	12	Q8QUT9	Q8qut9 infectious
50	35	9.0	42	6	O18958	O18958 bos taurus

#### ALIGNMENTS

RESULT 1

Q98TP9	Q98TP9	PRELIMINARY:	PRT;	40 AA.
AC	Q98TP9;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)			
DE	Metallothionein (MT) (Fragment).			
GN	MT.			
OS	Platichthys flesus (European flounder).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;			
OC	Pleuronectoidei; Pleuronectidae; Platichthys.			
OX	NCBI_TaxID=8260;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=OVARY;			
RA	Williams T.D., Chipman J.K.;			
RT	"A DNA array to monitor the effects of environmental pollution on			
RT	European flounder (Platichthys flesus).";			
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE			
CC	RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).			
CC	-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 1.			
CC	EMBL; AJ291833; CAC28138.1; ..			
DR	HSSP; P02795; IMHU.			
DR	InterPro; IPR003019; Metallthion.			
DR	InterPro; IPR000006; Metallthion_vert.			
DR	Pfam; PF00131; metalthio; 1.			
DR	PROSITE; PS00203; METALLOTHIONEIN_VRT; 1.			
FT	Chelation; Metal-binding; Metal-thiolate cluster.			
NON_TER	NON_TER	1	40	
NON_TER	NON_TER	1	40	







InterPro; IPR000347; Metallothion\_15.

2

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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*."  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AE003615; AAF52441.1; -  
 DR FlyBase; FBgn0042189; CG17376.  
 SQ SEQUENCE 45 AA; 4869 MW; F8F92B3B3FB8254 CRC64;

Query Match 10.2%; Score 40; DB 5; Length 45;  
 Best Local Similarity 25.0%; Pred. No. 4.8e+02;  
 Matches 10; Conservative 5; Mismatches 19; Indels 6; Gaps 1;

QY 5 GLGGRKCPSPNEIFSRCD-----GRQFCFQPNVVPKPLC 38  
 | | | | : : : : | : | | | |  
 Db 6 GCCGSPCPRRYLVNKNAPCVMCAPKRAHCYNTPPKCC 45

## RESULT 19

Q94214 ID Q94214 PRELIMINARY; PRT; 35 AA.

AC Q94214; DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE P0455H0310.11 protein.  
 GN P0455H0310.11  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MATSUMOTO T., Yamamoto K.;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0455H0310.";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP003435; BAB68022.1; -  
 SQ SEQUENCE 35 AA; 3068 MW; C6F1E2AB366A6B51 CRC64;

Query Match 10.0%; Score 39; DB 10; Length 35;  
 Best Local Similarity 58.3%; Pred. No. 5.2e+02;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GFGGLGGRGKC 12  
 | | | | |  
 Db 24 GGAAGCGSGGC 35

## RESULT 20

Q8XTX4 ID Q8XTX4 PRELIMINARY; PRT; 42 AA.

AC Q8XTX4; DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein RSC3422.  
 GN RSC3422 OR RS01802.  
 OS Ralstonia solanacearum (Pseudomonas solanacearum).  
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;  
 OC Ralstonia.  
 OX NCBI\_TaxID=305;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GM11000;  
 RX MEDLINE=21681879; PubMed=11823852;  
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
 RA Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,  
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
 RA Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,  
 RA Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*."  
 RL Nature 415:497-502(2002).  
 DR EMBL; AL646075; CAD16919.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 42 AA; 4646 MW; FD0483199B20FD51 CRC64;

Query Match 10.0%; Score 39; DB 16; Length 42;  
 Best Local Similarity 38.5%; Pred. No. 6.1e+02;  
 Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 17 IFSRCDGRCORFC 29  
 : : | | | : : : |  
 Db 8 LWSGCDGKAEQSC 20

## RESULT 21

Q8W2G7 ID Q8W2G7 PRELIMINARY; PRT; 38 AA.

AC Q8W2G7; DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE 4-hydroxyphenylpyruvate dioxygenase (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. TAINONG 67; TISSUE=LEAF;  
 RX MEDLINE=21326245; PubMed=11432928;  
 RA Lee R.H., Wang C.H., Huang L.T., Chen S.C.;  
 RT "Leaf senescence in rice plants: cloning and characterization of  
 RT senescence up-regulated genes.";  
 RL J. Exp. Bot. 52:1117-1121(2001).  
 DR EMBL; AP251065; AAL65390.1; -  
 KW Dioxygenase; Pyruvate.  
 FT NON\_TER  
 SQ SEQUENCE 38 AA; 4037 MW; 627174633993A0FE CRC64;

Query Match 9.7%; Score 38; DB 10; Length 38;  
 Best Local Similarity 53.3%; Pred. No. 7.6e+02;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 GGLGGRKCPSPNEIF 18  
 | | | | | : | |  
 Db 3 GCGGFGKGNFSELF 17

## RESULT 22

Q9MRL7 ID Q9MRL7 PRELIMINARY; PRT; 42 AA.

AC Q9MRL7; DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Putative ribulose-phosphate 3-epimerase (Fragment).  
 GN RPE.  
 OS Daucus carota (Carrot).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.  
 OX NCBI\_TaxID=4039;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. ST. VALERY; TISSUE=CALLUS;  
 RA Boschi E., Filippini F., Lo Schiavo F., Terzi M., Vergara R.;  
 RT "Identification of differential transcripts in auxinR lines of *Daucus  
 RT carota* L.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ297425; CAB97126.1; -

DR HSSP: Q43843: 1RPX.  
 DR InterPro: IPR000056; Ribul\_P\_3\_epim.  
 DR Pfam: PF00834; Ribul\_P\_3\_epim: 1.  
 DR PROSITE: PS01085; RIBUL\_P\_3\_EPIMER\_1; 1.  
 KW Chloroplast.  
 FT NON\_TER 1 1  
 FT NON\_TER 42 42  
 SQ SEQUENCE 42 AA: 4579 MW: 0EA026C8F51E14F3 CRC64;  
 Query Match 9.6%; Score 37.5; DB 8; Length 42;  
 Best Local Similarity 39.1%; Pred. No. 9.7e+02;  
 Matches 9; Conservative 2; Mismatches 9; Indels 3; Gaps 1;  
 QY 22 DGRCORFCNVVPKPLKICAP 44  
 DB 12 DG---RFPVNITIGPLVDALRP 31  
 RESULT 23  
 Q9UD12 PRELIMINARY; PRT: 33 AA.  
 AC Q9UD12: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE AMGX protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95322983; PubMed=7599636;  
 RA Lench N.J., Winter G.B.;  
 RT "Characterisation of molecular defects in X-linked amelogenesis imperfecta (ATH1)."  
 RT Hum. Mutat. 5:251-259(1995).  
 RL InterPro: IPR001230; Pfam: site.  
 DR PROSITE: PS00294; PRNylation; UNKNOWN\_1.  
 SQ SEQUENCE 33 AA: 3681 MW: D131F784BD7D8C93 CRC64;  
 Query Match 9.5%; Score 37; DB 4; Length 33;  
 Best Local Similarity 30.8%; Pred. No. 9e+02;  
 Matches 8; Conservative 3; Mismatches 15; Indels 0; Gaps 0;  
 QY 41 ICAPGCVCRGLYLRNKKKVCVPRSK 66  
 DB 5 LCTPCSPCRHSHLCRLCSPCLPC 30  
 RESULT 24  
 Q99PH5 PRELIMINARY; PRT: 41 AA.  
 AC Q99PH5: 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Insulinoma associated-2 (Fragment).  
 GN PTPN OR IA-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SVJ;  
 RX MEDLINE=21012487; PubMed=11126414;  
 RA Saeki K., Xie J., Notkins A.L.;  
 RT "Genomic structure of mouse IA-2: comparison with its human homologue."  
 RL Diabetologia 43:1429-1434(2000).  
 DR EMBL: AF288816; AAK07090.1; -;  
 DR MGD: MGI:102765; Ptpn.

FT NON\_TER 41  
 SQ SEQUENCE 41 AA: 4018 MW: BDD29522E5247C43 CRC64;  
 Query Match 9.5%; Score 37; DB 11; Length 41;  
 Best Local Similarity 70.0%; Pred. No. 1.1e+03;  
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GFGFGLGGRG 10  
 DB 8 GSGSGSGSG 17  
 RESULT 25  
 Q9W4K6 PRELIMINARY; PRT: 43 AA.  
 AC Q9W4K6: 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE CG12687 protein.  
 GN CG12687.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA Sutton R.G., Mortman J.R., Richards S., Ashburner M., Henderson S.N.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Zhang Q., Chen L.X.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de  
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
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 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
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 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
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 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M., M.G.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003431; AAF45945.1; -;  
 DR FlyBase: FBgn0040908; CG12687.  
 SQ SEQUENCE 43 AA: 4461 MW: 4A22167D4CFBAE45 CRC64;  
 Query Match 9.5%; Score 37; DB 5; Length 43;



Thu Feb 27 09:12:58 2003

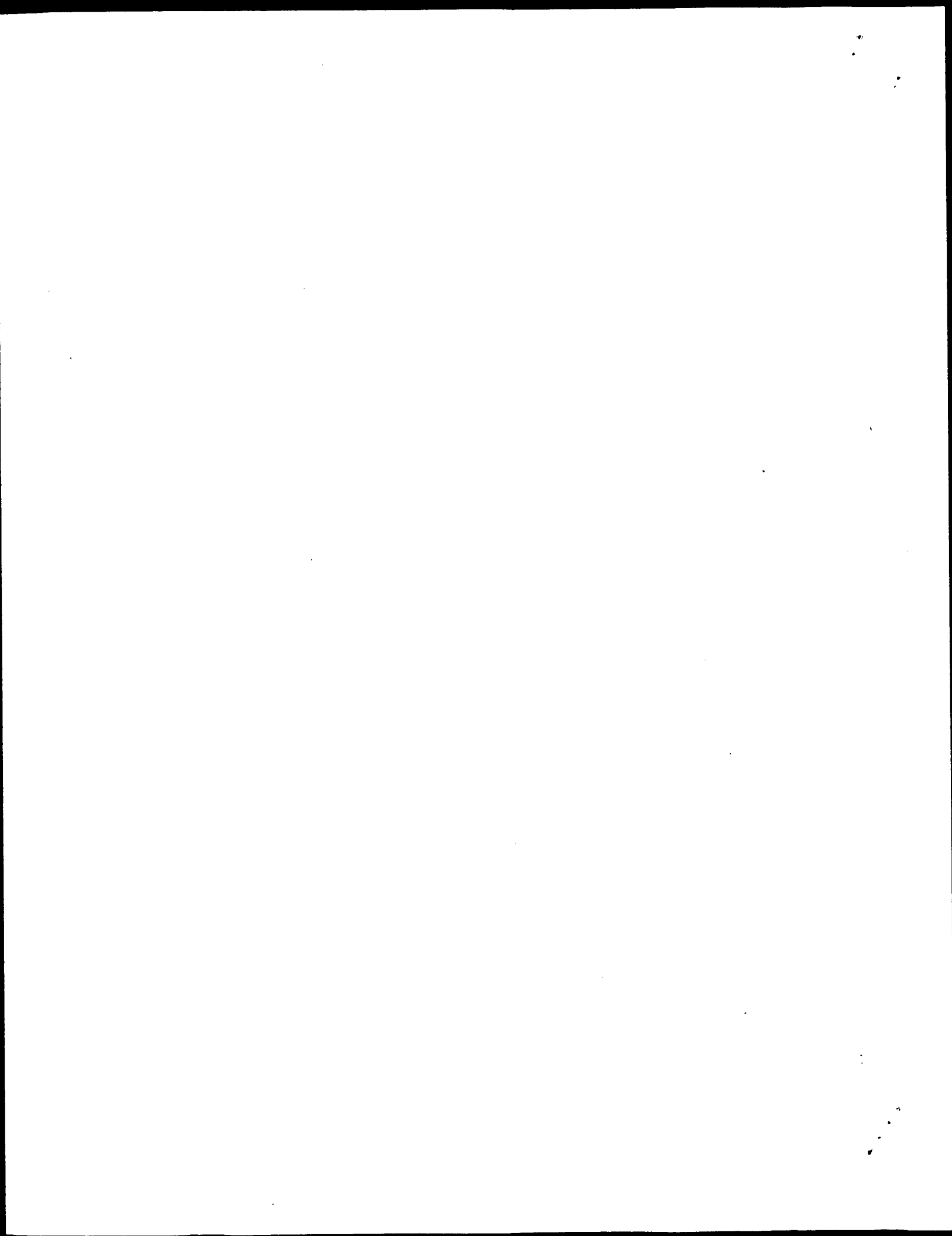
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Page 9

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Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 24 RCORFCFNVVP 34  
Db 3 KCLRFCVGTIP 13

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Job time : 32 secs



GenCore version 5.1.3  
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COM protein - protein search, using sw model

Run on: February 27, 2003, 09:03:04 ; Search time 33 Seconds  
(without alignments)  
270.539 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

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Total number of hits satisfying chosen parameters: 63089

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Maximum DB seq length:	45

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	62	15.9	43	22	AAB60286	Human factor IX (h
2	58.5	15.0	39	20	AAV02082	KIX peptide used t
3	57	14.6	40	5	AAP40692	Sequence encoded b
4	57	14.6	40	5	AAP40220	Partial sequence o
5	53	13.6	38	22	AAB95640	Human testicular a
6	53	13.6	38	22	AAW94179	Human reproductive
7	52.5	13.4	36	23	AAU91021	Transplant media a
8	51	13.0	32	17	AAW12303	Modified ligand sp
9	50	12.8	32	21	AAV59107	N. clavipes spider
10	50	12.8	38	20	AAV02077	Kalio toxin peptide

11	49	12.5	38	20	AAV02081	KTX peptide used t
12	49	12.5	40	23	AAU91037	Transplant media a
13	49	12.5	42	19	AAW48751	T-cell surface ant
14	49	12.5	45	21	AAV98018	Human growth hormo
15	48.5	12.4	34	22	AAO09332	Human polypeptide
16	48.5	12.4	42	9	AAP82390	KM-2 antiviral and
17	48.5	12.4	44	22	AAO09473	Human polypeptide
18	48	12.3	37	22	AAB92225	Toxin peptide SEQ
19	48	12.3	37	22	AAB92226	Toxin peptide SEQ
20	48	12.3	40	15	AAR63519	Bovine neutrophil
21	48	12.3	41	23	AAU91032	Transplant media a
22	48	12.3	41	22	AAAB84562	Amino acid sequenc
23	48	12.3	42	22	AAB84567	Amino acid sequenc
24	47	12.0	39	18	AAV31658	Nisin-subtilin chi
25	47	12.0	39	22	ABG23312	Novel human diagno
26	47	12.0	45	18	AAW10163	Alpha-hordothionin
27	47	12.0	45	19	AAW141690	Methionine substit
28	46.5	11.9	38	20	AAV02080	Agitoxin peptide u
29	46.5	11.9	38	21	AAV83190	IRK1 Agitoxin2 lig
30	46.5	11.9	41	22	ABBA0595	Peptide #8101 enco
31	46.5	11.9	41	22	AAW61453	Human brain expres
32	46.5	11.9	41	22	AAW74243	Human bone marrow
33	46.5	11.9	41	22	AAW34355	Peptide #8392 enco
34	46	11.8	32	19	AAW75704	Metal binding prot
35	46	11.8	33	19	AAW53350	Nephila clavipes s
36	46	11.8	33	21	AAV59074	N. clavipes spider
37	46	11.8	42	22	AAO13358	Human polypeptide
38	46	11.8	43	22	ABG28039	Novel human diagno
39	46	11.8	43	22	AAU14870	Novel bone marrow
40	46	11.8	45	14	AAR42283	Corticostatin. Sy
41	45.5	11.6	40	22	AAO02434	Human polypeptide
42	45.5	11.6	41	20	AAV27030	Amino acid sequenc
43	45	11.5	32	17	AAW12904	Modified ligand sp
44	45	11.5	33	22	AAW91722	Human immune/haema
45	45	11.5	39	18	AAW24383	Gallinacin 1. Gal
46	45	11.5	45	15	AAR60047	Alpha-hordothionin
47	45	11.5	45	15	AAR60051	Alpha-hordothionin
48	45	11.5	45	15	AAR60052	Alpha-hordothionin
49	45	11.5	45	19	AAW58555	High lysine deriva
50	44.5	11.4	35	22	AAO05239	Human polypeptide

## ALIGNMENTS

RESULT 1  
AAB60286

ID	AAB60286	standard	Protein: 43 AA.
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3	3	3	3
4	4	4	4
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6	6	6	6
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10	10	10	10
11	11	11	11
12	12	12	12
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17	17	17	17
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99	99	99	99
100	100	100	100

AA  
AC AAB60286:

XX  
DT 30-MAR-2001 (first entry)

Human factor IX (hFIX) exon-encoded fragment, SEQ ID NO:9.

Age-related gene regulation; liver-specific; gene expression;

KW human factor IX; hFIX; AE5'; AE3'; age-regulatable expression construct;

antisenese therapy; gene therapy; thrombosis; cardiovascular disease; KW

KW  
diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis;  
KW  
antense therapy; gene therapy; thrombosis; cardiovascular disease;

diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia.

XX Homo sapiens.

XX  
PN  
WO200075279-A2.XX  
BD 14-DEC-2000

14 DEC 2000;  
06-JUN-2000: 2000WO-US15728

06-JUN-2000; 2000WO-0515728.  
XX  
06-JUN-2000; 2000WO-0339935

PR 09-JUN-1999; 99US-03  
XX

PA  
YV



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XX PD 16-FEB-1984.
XX PF 03-AUG-1983; 83WO-GB00191.
XX PR 06-MAY-1983; 83GB-0012491.
XX PR 04-AUG-1982; 82GB-0022485.
XX PA (NATR ) NATIONAL RES DEV CORP.
XX PA (BROW/) BROWNLEE G G.
XX PT Brownlee G, Choo KH;
XX DR WPI; 1984-049331/08.
XX DR N-PSDB; AAN40141.
XX PT Recombinant DNA cloning vehicles - useful in prodn. of factor IX
XX PT polypeptide and of diagnostic probes for Christmas disease
XX PS Example; Fig 7a-i; 7lpp; English.
XX CC The inventors claim DNA molecules comprising part or all of the
XX CC human factor IX DNA. The invention also includes cDNA derived from
XX CC human factor IX RNA. Specifically claimed are: recombinant DNA (the
XX CC phage present in clone lambda HIX-1) deposited as NCIB No. 11749;
XX CC Recombinant DNA in which the cloning vehicle is the modified PAT 153
XX CC plasmid present in E.coli NCIB No. 11747; Recombinant DNA in which
XX CC the bovine factor IX DNA sequence is contained in the recombinant
XX CC DNA transformed into E.coli to form a clone deposited as NCIB No.
XX CC 11748.
XX SQ Sequence 40 AA;

Query Match 14.6%; Score 57; DB 5; Length 40;
Best Local Similarity 32.5%; Pred. No. 78;
Matches 13; Conservative 5; Mismatches 14; Indels 8; Gaps 2;

QY 22 DGRCOREFCPNVVPKPLCIKICAPGCVCRIGY-LRNKKKVC 60
Db :||||:| | | | | | | | | | | | | | | | | |
8 NGRCEQFCNKSADNKVV-----CSCTEGYRLAENQKSC 40

RESULT 4
AAP40220
ID AAP40220 standard; Protein; 40 AA.
AC AAP40220;
XX DT 13-FEB-1992 (first entry)
XX DE Partial sequence of human factor IX (starting AA no. 85) encoded
XX DE by an exon of human factor IX genomic DNA.
XX KW Haemophilia; Christmas disease; diagnosis; treatment.
XX OS Homo sapiens.
XX PN GB2125409-A.
XX PD 07-MAR-1984.
XX PF 03-AUG-1983; 83GB-0020975.
XX PR 16-MAY-1983; 83GB-0012490.
XX PR 04-AUG-1982; 82GB-0022486.
XX PR 03-AUG-1983; 83GB-0020975.
XX PA (NATR ) NATIONAL RES DEV CORP.
XX PL Brownlee GG, Choo KH;
XX DR WPI; 1984-057898/10.
XX DR N-PSDB; AAN40176.

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XX Prodn. of artificial human factor IX - by use of recombinant DNA
XX PT sequences for host transformation and cultivation
XX PS Example; Fig 7; 49pp; English.
XX CC The inventors claim a recombinant DNA having a human factor IX
XX CC sequence pref. at least 50 nucleotides long, esp. 75-27000
XX CC nucleotides. A cloning vector contg. foreign DNA is also claimed.
XX CC The foreign sequence pref. includes the whole of an exon sequence of
XX CC the human factor IX genome. The cloning vehicle may be a modified
XX CC PAT 153 plasmid. Also claimed is a labelled diagnostic probe
XX CC comprising a DNA molecule having a single- or double-stranded probe
XX CC sequence of 15 to 10000 nucleotides long Factor IX DNA sequence.
XX SQ Sequence 40 AA;

Query Match 14.6%; Score 57; DB 5; Length 40;
Best Local Similarity 32.5%; Pred. No. 78;
Matches 13; Conservative 5; Mismatches 14; Indels 8; Gaps 2;

QY 22 DGRCOREFCPNVVPKPLCIKICAPGCVCRIGY-LRNKKKVC 60
Db :||||:| | | | | | | | | | | | | | | | | |
8 NGRCEQFCNKSADNKVV-----CSCTEGYRLAENQKSC 40

RESULT 5
ABB95640
ID ABB95640 standard; Protein; 38 AA.
XX AC ABB95640;
XX DT 21-JUN-2002 (first entry)
XX DE Human testicular antigen SEQ ID NO: 1024.
XX KW Human; testicular antigen; testes; cancer; metastasis; immune disorder;
XX KW reproductive system disorder; urinary system disorder; gene therapy;
XX KW cardiovascular disorder; respiratory disorder; neurological disorder;
XX KW gastrointestinal disease; infection; cytostatic.
XX OS Homo sapiens.
XX PN WO200155317-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01329.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
XX PR 30-JUN-2000; 2000US-0215135.
XX PR 07-JUL-2000; 2000US-0216647.
XX PR 07-JUL-2000; 2000US-0216880.
XX PR 11-JUL-2000; 2000US-0217487.
XX PR 11-JUL-2000; 2000US-0217496.
XX PR 14-JUL-2000; 2000US-0218290.
XX PR 26-JUL-2000; 2000US-0220963.
XX PR 26-JUL-2000; 2000US-0220964.
XX PR 14-AUG-2000; 2000US-0224518.
XX PR 14-AUG-2000; 2000US-0224519.
XX PR 14-AUG-2000; 2000US-0225213.
XX PR 14-AUG-2000; 2000US-0225214.
XX PR 14-AUG-2000; 2000US-0225266.
XX PR 14-AUG-2000; 2000US-0225267.

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PR	14-AUG-2000;	2000US-0225268.	PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000;	2000US-0225270.	PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000;	2000US-0225447.	PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000;	2000US-0225757.	PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000;	2000US-0225758.	PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000;	2000US-0225759.	PR	08-NOV-2000;	2000US-0246611.
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PR	18-AUG-2000;	2000US-0226279.	PR	17-NOV-2000;	2000US-0249207.
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PR	22-AUG-2000;	2000US-0226868.	PR	17-NOV-2000;	2000US-0249209.
PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249210.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249211.
PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249212.
PR	01-SEP-2000;	2000US-0229287.	PR	17-NOV-2000;	2000US-0249213.
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PR	08-SEP-2000;	2000US-0231414.	PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000;	2000US-0232080.	PR	01-DEC-2000;	2000US-0250160.
PR	08-SEP-2000;	2000US-0232081.	PR	01-DEC-2000;	2000US-0250391.
PR	12-SEP-2000;	2000US-0231968.	PR	05-DEC-2000;	2000US-0251030.
PR	14-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251988.
PR	14-SEP-2000;	2000US-0232398.	PR	05-DEC-2000;	2000US-0256719.
PR	14-SEP-2000;	2000US-0232399.	PR	06-DEC-2000;	2000US-0256719.
PR	14-SEP-2000;	2000US-0232401.	PR	06-DEC-2000;	2000US-0251479.
PR	14-SEP-2000;	2000US-0233063.	PR	08-DEC-2000;	2000US-0251856.
PR	14-SEP-2000;	2000US-0233064.	PR	08-DEC-2000;	2000US-0251868.
PR	14-SEP-2000;	2000US-0233065.	PR	08-DEC-2000;	2000US-0251869.
PR	21-SEP-2000;	2000US-0234223.	PR	08-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	2000US-0234274.	PR	08-DEC-2000;	2000US-0251990.
PR	25-SEP-2000;	2000US-0234997.	PR	11-DEC-2000;	2000US-0254097.
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PR	26-SEP-2000;	2000US-0235484.	XX		
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PR	27-SEP-2000;	2000US-0235836.	XX		
PR	29-SEP-2000;	2000US-0236327.	XX		
PR	29-SEP-2000;	2000US-0236367.	DR		
PR	29-SEP-2000;	2000US-0236368.	XX		
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PR	29-SEP-2000;	2000US-0236370.	PT		
PR	02-OCT-2000;	2000US-0236802.	PT		
PR	02-OCT-2000;	2000US-0237037.	XX		
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PR	13-OCT-2000;	2000US			

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AC AAM94179;  
XX 21-NOV-2001 (first entry)  
DT Human reproductive system related antigen SEQ ID NO: 2837.  
XX Human; reproductive system related antigen; reproductive system disorder;  
KW cancer; gene therapy.  
XX Homo sapiens.  
XX WO200155320-A2.  
PD 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01339.  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
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PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.

PS Claim 8; Page 29; 78pp; English.

XX The invention describes new transplant compositions comprising

CC antimicrobial polypeptides or pore forming agents and/or cell surface

CC receptor binding compounds. The media is capable of extending the

CC preservation period past 72 hours and can provide organs with increased

CC functionality upon transplant. Animals receiving kidneys stored in the

CC media of the present invention for either three or four days had serum

CC creatinine levels of less than half of those observed in control animals

CC receiving kidneys stored in UW solution (defined in the specification)

CC alone. Lower serum creatinine levels are indicative of healthier kidneys

CC and a more preferable prognosis for the transplant patient. The media of

CC the invention are useful for decreasing the incidence and/or severity of

CC delayed graft function in patients receiving transplanted kidneys stored

CC and/or treated in the media. The media may also be used in procedures

CC such as cardioplegia. It is contemplated that transplant of healthier

CC organs leads to a decrease in chronic rejection. This sequence represents

CC an antimicrobial defensin peptide studied in the development of the

CC transplant media.

XX

SQ Sequence 36 AA;

Query Match 13.4%; Score 52.5; DB 23; Length 36;

Best Local Similarity 27.7%; Pred. No. 2e+02;

Matches 13; Conservative 4; Mismatches 17; Indels 13; Gaps 2;

QY 2 GFGGLGRGKCPSEIFSRDGRCPNVVVKPLCIKICAPGVCV 48

DB 1 GFG-----CPFNQ-----GACHRHCRSIRRGYCGAGLFGKQTC 34

RESULT 8

AAW12903

ID AAW12903 standard; peptide; 32 AA.

AC AAW12903;

DT 15-APR-1997 (first entry)

DE Modified ligand specific for EGF receptor.

XX Class I receptor tyrosine kinase; RTK; ligand; bridge; prebridge;

KW domain; subdomain; beta-turn; malignancy; aberrant expression;

KW EGF; epidermal growth factor.

XX Synthetic.

XX Key Location/Qualifiers

FT Domain 1..6

FT Disulfide-bond 6..14

FT Domain 7..13

FT /label= bridge\_domain

FT /note= "this bridge contains a beta-turn

FT corresponding to that present within

FT domain B of native EGF"

FT Region 7..10

FT /label= prebridge\_subdomain

FT Region 11..13

FT /label= bridge\_subdomain

FT Domain 14..32

FT /label= domain\_C1

FT Disulfide-bond 16..25

XX WO9623883-A2.

XX 08-AUG-1996.

XX 02-FEB-1996; 96WO-US01465.

XX 02-FEB-1995; 95US-0384714.

XX (BERL-) BERLEX LAB INC.

PS Claim 11; SEQ ID NO 2837; 1297pp + Sequence Listing; English.

XX The present invention provides the protein and coding sequences of a

CC number of human reproductive system related antigens. These can be used

CC in the prevention and treatment of reproductive system disorders,

CC including cancer. The present sequence is a protein of the invention.

XX

SQ Sequence 38 AA;

Query Match 13.6%; Score 53; DB 22; Length 38;

Best Local Similarity 35.6%; Pred. No. 1.9e+02;

Matches 16; Conservative 5; Mismatches 14; Indels 10; Gaps 3;

QY 6 LGGRGKCPSEIFSRDGRCPNVVVKPLCIKICAPGVCVRL 50

DB 2 LDARASWFSNQL---CDLR-----QVIP-ALCFICSGMGI 36

RESULT 7

AAU91021

ID AAU91021 standard; Peptide; 36 AA.

AC AAU91021;

DT 05-JUN-2002 (first entry)

DE Transplant media associated defensin peptide #22.

XX Transplant; antimicrobial peptide; pore forming agent;

KW cell surface receptor binding compound; kidney transplant;

KW cardioplegia; organ transplant; transplant rejection; defensin.

XX Androctonus australis hector.

OS WO200209738-A1.

PN 07-FEB-2002.

XX 27-JUL-2001; 2001WO-US23785.

XX 28-JUL-2000; 2000US-221632P.

PR 17-NOV-2000; 2000US-249602P.

PR 15-MAY-2001; 2001US-290932P.

XX (MURP/) MURPHY C J.

XX Murphy CJ, Reid TW, Meanulty JF;

XX WPI: 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents

PT and/or cell surface receptor binding compounds useful for the storage

PT and preservation of organs prior to transplant .

XX



XX Harkins RN, Katz BA, Seto M;  
 XX WPI; 1996-371432/37.  
 XX Modified ligand specific for Class I receptor tyrosine kinase  
 XX used to quantify the presence of the kinase on human cells, and to  
 XX treat malignancy and aberrant expression  
 XX Claim 13; Page 44; 58pp; English.  
 XX Modified ligand specific for a Class I receptor tyrosine kinase (RTK)  
 XX and corresponding to a native RTK ligand with amino acids forming 3 Cys  
 XX linkages is claimed. In the native RTK ligand these linkages define  
 XX domains A, B and C resp. and have 6 Cys residues, with the first linkage  
 XX being between Cys1 and Cys3, the second between Cys2 and Cys4, and  
 XX the third between Cys5 and Cys6. Domain A is Cys1, Cys2 and the amino  
 XX acids between; domain B is the amino acids between Cys2 and Cys4; and  
 XX domain C is Cys4 and the amino acids attached to the C-terminal of Cys4.  
 XX The new modified RTK ligand has 4 Cys residues forming 2 linkages  
 XX between Cys2 and 4 and Cys5 and 6 resp., and has 2 domains, A1 and C1,  
 XX corresponding to domains A and C resp. of the native ligand and contg.  
 XX the biologically active amino acids of these domains. Cys 2, which is  
 XX the C-terminus of domain A1, and Cys 4, which is the N-terminus of C1,  
 XX are connected by a peptide bridge comprising a prebridge subdomain and  
 XX a bridge subdomain. Within the peptide bridge there is a beta turn  
 XX corresponding to that present within domain B of the native RTK ligand.  
 XX The modified ligand is used to quantify the presence of RTKs on a human  
 XX cell, and to treat malignancy and aberrant expression. It may have  
 XX agonist or antagonist activity. The modified ligand can be labelled  
 XX easily to provide a rapid assay for the presence or absence of RTKs on  
 XX particular cells.  
 XX The present sequence is one of 10 specific examples of the new ligands  
 XX directed towards the EGF receptor.

XX Sequence 32 AA;

Query Match 13.0%; Score 51; DB 17; Length 32;  
 Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 38 CIKICAPGCVCRIGYL 53  
 I :||||| I:  
 Db 6 CPHGTSPGCVCHSGYV 21

RESULT 9  
 AAY59107  
 ID AAY59107 standard; peptide; 32 AA.

XX AAY59107;

XX 08-MAR-2000 (first entry)

DE N. clavipes spider silk protein 1 repeat fragment.

XX Spider silk protein; dragline silk protein; fiber.

XX Nephila clavipes.

XX US5989894-A.

XX 23-NOV-1999.

XX 04-OCT-1994; 94US-0317844.

XX 15-APR-1991; 91US-0684819.

XX 20-APR-1990; 90US-0511792.

XX (UYWY-) UNIV WYOMING.

XX Hinman MB, Xu M, Lewis RV;

XX

DR WPI; 2000-061225/05.

XX Isolated DNA, vector and transformed cell encoding for and useful in  
 XX the production of spider silk protein

XX Claim 5; Columns 71-72; 65pp; English.

XX The invention provides isolated cDNA molecules coding for spider silk  
 XX proteins. The spider silk proteins are characterized by repeating alpha  
 XX and beta regions and optional variable regions. The DNA sequences are  
 XX useful in the production of spider silk protein by recombinant DNA  
 XX techniques. The recombinant spider silk proteins may be used for the  
 XX production of fibers. Sequences AAY59101-125 represent repeat fragments  
 XX of N. clavipes spider silk protein 1.

XX Sequence 32 AA;

Query Match 12.8%; Score 50; DB 21; Length 32;  
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;  
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFGGGLGGRG 10  
 II:||||| I:  
 Db 23 GGYGGLGGGG 32

RESULT 10

AAY02077

ID AAY02077 standard; peptide; 38 AA.

XX AAY02077;

XX 06-JUL-1999 (first entry)

XX Kaliotoxin peptide used to block potassium channels.

XX Neuronal potassium channel; Kv1.1; Kv1.2; Kv1.3; neurological disorder;  
 XX immune disorder; nerve signal transmission; block; multiple sclerosis;  
 XX cerebral; medullary inflammatory disorder; Baló; Devic; disseminated;  
 XX haemorrhagic acute encephalitis; optic neuropathy; systemic disease;  
 XX Behcet; sarcoidosis; vasculitis; peripheral inflammatory disorder;  
 XX polyradiculoneuritis; infection; collagenosis; neurodegenerative disease;  
 XX amyotrophic lateral sclerosis; metabolic disorder; vascular ischaemia;  
 XX tumour; trauma.

XX Synthetic.

XX FR2769226-A1.

XX 09-APR-1999.

XX 06-OCT-1997; 97FR-0012421.

XX 06-OCT-1997; 97FR-0012421.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Beraud E, Crest M, Gola M, Van Rietschoten J;

XX WPI; 1999-246903/21.

XX Use of neuronal potassium channel blockers, especially kaliotoxin  
 XX peptides - to prepare therapeutic compositions for treatment of  
 XX neurological disorders

XX Claim 8; Page 19; 30pp; French.

XX The specification describes the use of compounds that block neuronal  
 XX potassium channels of the Kv1.1, Kv1.2 and optionally Kv1.3 type to  
 XX prepare therapeutics for treating human or animal neurological  
 XX disorders, e.g. of immune origin, in which nerve signal transmission  
 XX is blocked. The products are especially used for treating multiple  
 XX sclerosis. Other uses are for treating other cerebral and medullary

disorders, e.g. of immune origin, in which nerve signal transmission is blocked. The products are especially used for treating multiple sclerosis. Other uses are for treating other cerebral and medullary inflammatory disorders, e.g. Balo, Devic, disseminated and haemorrhagic acute encephalitis, isolated optic neuropathies and central complications of systemic diseases (Behcet, sarcoidosis and other forms of vasculatits) and peripheral inflammatory disorders, e.g. acute and chronic polyradiculoneuritis, infection- and collagenosis-associated neuropathies, neurodegenerative diseases, especially amyotrophic lateral sclerosis, and other cerebral and medullary disorders associated with metabolic disorders, vascular ischaemia, tumours and trauma. The present sequence represents a peptide of the invention.

Query Match	12.5%	Score 49;	DB 20;	Length 38;
Best Local Similarity	29.2%;	Pred. NO. 4.6e+02;		
Mismatches	14;	Conservative	5;	Mismatches 17; Indels 12; Gaps 2

QY 16 EIFSRCDGRQRCQFCPNVVPKLCIKICAPGCVCRLGYLRNKKKVCVPR 63  
 3 EIFNVKSCGSYO-----CIKXCKDAGM--RFGKCMRKKCHCTPK 38

AAU91037  
ID AAU91037 standard: peptide: 40 AA:XX  
AC AAI91037:

DE KTX peptide used to block potassium channels.

XX	Transplant media associated defensin peptide #38.
DE	
XX	Transplant; antimicrobial peptide; pore forming agent;
KW	cell surface receptor binding compound; kidney transplant;
KW	cardioplegia; organ transplant; transplant rejection; defensin.
XX	
OS	Aedes aegypti.

XX	Key	Location/Qualifiers
FH		

XX	27-JUL-2001; 2001WO-US23785.
PF	
XX	
PR	28-JUL-2000; 2000US-221632P.
PR	17-NOV-2000; 2000US-249602P.
PR	15-MAY-2001; 2001US-290932P.

XX  
PT  
Murphy C.T. Reid TW

06-OCT-1997: 97ER-0012421.

Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.

XX  
PC  
claim 8: page 30: 78pp: English:

XX  
CC  
the invention describes new transplant compositions comprising

XX Use of neuronal potassium channel blockers, especially kaliotoxin  
PT peptides - to prepare therapeutic compositions for treatment of  
PT neurological disorders  
PT

The specification describes the use of compounds that block neuronal potassium channels of the Kv1.1, Kv1.2 and optionally Kv1.3 type to prepare therapeutics for treating human or animal neurological

The specification describes the use of compounds that block neuronal potassium channels of the Kv1.1, Kv1.2 and optionally Kv1.3 type to prepare therapeutics for treating human or animal neurological

The specification describes the use of compounds that block neuronal potassium channels of the Kv1.1, Kv1.2 and optionally Kv1.3 type to prepare therapeutics for treating human or animal neurological







intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.

Query Match 12.3%; Score 48; DB 22; Length 37;  
Best Local Similarity 29.8%; Pred. No. 5.7e+02;  
Matches 14; Conservative 4; Mismatches 17; Indels 12; Gaps 2;

RESULT 20  
AAR63519  
ID AAR63519 standard; peptide; 40 AA.

Query Match 12.3%; Score 48; DB 15; Length 40;  
Best Local Similarity 29.4%; Pred. No. 6.1e+02;  
Matches 10: Conservative 7; Mismatches 13; Indels 4; Gaps 1;

RESULT 21  
AAU91032  
ID AAU91032 standard; Peptide; 40 AA.

DE	Transplant media associated defensin peptide #33.
XX	
KW	Transplant; antimicrobial peptide; pore forming agent;
KW	cell surface receptor binding compound; kidney transplant;
KW	cardioplegia; organ transplant; transplant rejection; defensin.
XX	
XX	
OS	Bos taurus.
XX	
PN	WO200209738-A1.
XX	
PD	07-FEB-2002.
XX	
PF	27-JUL-2001; 2001WO-US23785.
XX	
XX	28-JUL-2000; 2000US-221632P.
PR	17-NOV-2000; 2000US-249602P.
PR	15-MAY-2001; 2001US-290932P.
XX	
PA	(MURP/) MURPHY C J.
XX	
PI	Murphy CJ, Reid TW, Mcanulty JF;
XX	
DR	WPI; 2002-268995/31.
XX	
PT	Media comprising antimicrobial polypeptides or pore forming agents
PT	and/or cell surface receptor binding compounds useful for the storage
PT	and preservation of organs prior to transplant -
XX	
PS	Claim 8; Page 29; 78pp; English.

```
Query Match      12.3%; Score 48; DB 23; Length 40;
Best Local Similarity 29.4%; Pred. No. 6.1e+02;
Matches 10: Conservative 7; Mismatches 13; Indels 4; Gaps 1;
```

RESULT 22	
AAAB84582	
ID	AAAB84582 standard; Protein; 41 AA.
XX	
XX	
AC	AAAB84582;
XX	
XX	
DD	05-SEP-2001 (first entry)
DE	Amino acid sequence of a mature chimpanzee EP2 peptide. .
XX	
XX	Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW	epithelial infection; epididymitis; urogenital tract infection;
KW	sexually transmitted disease; condom.
KW	

05-SEP-2001 (first entry)  
Amino acid sequence of a mature chimpanzee EP2 peptide.



PD 03-APR-1997.  
 XX 30-SEP-1996; 96WO-US15160.  
 XX 28-SEP-1995; 95US-0535494.  
 XX (UYMA-) UNIV MARYLAND BALTIMORE.  
 PA Hansen JN;  
 PI WPI; 1997-225847/20.  
 DR N-PSDB; AAX87828.  
 DR Lantibiotic mutants and chimera(s) - having enhanced stability and  
 PT activity compared to nisin  
 XX Example; Fig 2; 60pp; English.  
 PS The present sequence represents a chimeric lantibiotic pre-peptide  
 CC composed of a subtilin leader region and a nisin-subtilin fusion  
 CC comprising residues 1-11 of Lactococcus lactis nisin and residues  
 CC 12-32 of Bacillus subtilis subtilin. DNA (see AAX87828) encoding the  
 CC chimera was produced by mutagenesis of subtilin DNA such that  
 CC residues 1, 2 and 4 of subtilin were replaced by the corresponding  
 CC residues of nisin. The chimera was efficiently processed in B.  
 CC subtilis into a functional lantibiotic. Post-translational  
 CC modifications included the dehydration of serine and threonine  
 CC residues and formation of thioether crosslinkages. The chimera had  
 CC similar activity to nisin with respect to activity against Bacillus  
 CC cereus spores and vegetative cells. The chimera can be produced by  
 CC cultivation of transformed host cells and used e.g. as a food  
 CC preservative to treat, kill or inhibit the growth of microorganisms  
 CC and/or their spores.  
 XX  
 SQ Sequence 39 AA;  
 Query Match 12.0%; Score 47; DB 18; Length 39;  
 Best Local Similarity 43.8%; Pred. No. 7.5e+02;  
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
 OY 32 VVPKPLCIKICAPGV 47  
 : : : : :  
 Db 4 ITPQITSISLCTPGCV 19  
 RESULT 25  
 ABG23312  
 ID ABG23312 standard; Protein; 39 AA.  
 XX  
 AC ABG23312;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #23303.  
 XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US08631.  
 XX  
 PR 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;  
 XX

DR WPI; 2001-639362/73.  
 DR N-PSDB; AAS87499.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX  
 PS Claim 20: SEQ ID NO 53671; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes.  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG0377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 39 AA;  
 Query Match 12.0%; Score 47; DB 22; Length 39;  
 Best Local Similarity 29.4%; Pred. No. 7.5e+02;  
 Matches 15; Conservative 5; Mismatches 5; Indels 26; Gaps 4;  
 OY 19 SRCD-CRCQRF-----CPNVVFKPLCIKICAPGVCRLL-----GYLRN 55  
 : : : : :  
 Db 1 SKCSIGLYORYPYSGNCXN-----SGCICRYVXCCEHRYGVN 39

Search completed: February 27, 2003, 09:04:23  
 Job time : 35 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 27, 2003, 09:04:28 : Search time 13 seconds  
(without alignments)  
194.412 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGFGLGGRGKPSNEIFSR.....CRLGVLRNKKKVCVPRSKCG 67

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174566 segs, 37721826 residues

Total number of hits satisfying chosen parameters: 8992

Minimum DB seq length: 32

Maximum DB seq length: 45

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpa/PCTUS\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubpa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55.5	14.2	38	10	US-09-847-185-47
2	55.5	14.2	45	9	US-10-136-573A-11
3	55.5	14.2	45	9	US-09-877-665-11
4	55.5	14.2	45	9	US-10-215-862-11
5	55.5	14.2	45	10	US-09-817-647-11
6	49	12.5	40	10	US-09-917-340-73
7	48	12.3	40	10	US-09-917-340-68
8	47.5	12.1	42	10	US-09-865-578-4
9	46.5	11.9	41	10	US-09-864-761-44588
10	46	11.8	37	10	US-09-829-481-11
11	46	11.8	37	10	US-09-917-340-57
12	45	11.5	45	9	US-10-136-573A-13
13	45	11.5	45	9	US-09-877-665-13
14	45	11.5	45	9	US-10-215-862-13
15	45	11.5	45	10	US-09-817-647-13
16	44	11.3	34	10	US-09-040-518-2
17	44	11.3	38	10	US-09-030-619-200
18	44	11.3	40	12	US-10-124-557-8
19	43.5	11.1	37	9	US-09-814-452-5

20	43.5	11.1	45	9	US-10-136-573A-16	Sequence 16, Appl
21	43.5	11.1	45	9	US-09-877-665-16	Sequence 16, Appl
22	43.5	11.1	45	9	US-10-215-862-16	Sequence 16, Appl
23	43.5	11.1	45	10	US-09-817-647-16	Sequence 16, Appl
24	43	11.0	38	10	US-09-030-619-197	Sequence 16, Appl
25	43	11.0	45	10	US-09-759-584-41	Sequence 17, App
26	42.5	10.9	34	1	US-08-841-636A-37	Sequence 37, Appl
27	42.5	10.9	35	10	US-09-894-882-415	Sequence 41, Appl
28	42.5	10.9	36	10	US-09-894-882-4	Sequence 415, App
29	42	10.7	33	10	US-09-864-761-35732	Sequence 4, Appli
30	42	10.7	34	10	US-09-864-761-40433	Sequence 35732, A
31	42	10.7	41	12	US-10-124-557-6	Sequence 40433, A
32	41.5	10.6	35	10	US-09-864-761-44585	Sequence 6, Appli
33	41.5	10.6	44	10	US-09-879-666-7	Sequence 44585, A
34	41	10.5	34	10	US-09-854-864-7	Sequence 7, Appli
35	41	10.5	38	10	US-09-864-761-41960	Sequence 7, Appli
36	41	10.5	42	8	US-08-969-137-3	Sequence 41960, A
37	40.5	10.4	32	9	US-09-984-245-276	Sequence 3, Appli
38	40.5	10.4	38	10	US-09-917-340-58	Sequence 276, App
39	40.5	10.4	45	9	US-10-086-176A-1	Sequence 58, Appl
40	40	10.2	32	9	US-09-749-637A-146	Sequence 1, Appli
41	40	10.2	37	9	US-09-814-452-4	Sequence 146, App
42	40	10.2	37	9	US-09-814-452-26	Sequence 4, Appli
43	40	10.2	41	10	US-09-864-761-43897	Sequence 26, Appl
44	39.5	10.1	35	9	US-10-044-359-26	Sequence 43897, A
45	39.5	10.1	36	10	US-09-894-882-3	Sequence 26, Appl
46	39.5	10.1	40	9	US-10-125-459-13	Sequence 3, Appli
47	39.5	10.1	40	9	US-10-067-761-26	Sequence 13, Appl
48	39.5	10.1	40	10	US-09-804-156-26	Sequence 26, Appl
49	39.5	10.1	40	10	US-09-946-633-13	Sequence 13, Appl
50	39	10.0	36	9	US-09-916-494A-8	Sequence 8, Appli

## ALIGNMENTS

## RESULT 1

US-09-847-185-47  
: Sequence 47, Application US/09847185  
: Patent No. US2002076392A1  
: GENERAL INFORMATION:  
: APPLICANT: Soo Hoo, William  
: TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
: RESPONSE USING SAME  
: NUMBER OF SEQUENCES: 50  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: CAMPBELL & FLORES, LLP  
: STREET: 4370 La Jolla Village Drive, Suite 700  
: CITY: San Diego  
: STATE: California  
: COUNTRY: United States  
: ZIP: 92121

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/847,185  
FILING DATE: 01-May-2001  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 09/201,931  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IM 2442  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949  
INFORMATION FOR SEQ ID NO: 47:

```

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-847-185-47

Query Match 14.2%; Score 55.5; DB 10; Length 38;
Best Local Similarity 29.8%; Pred. No. 27;
Matches 14; Conservative 0; Mismatches 14; Indels 19; Gaps 2;

Qy 2 GFGGLGRGKPCSPNEIFSRCDGRCPNVVVKPLCIKICAPGVC 48
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GCGGAGGGGCC-----CTAGC-----ACCCACCGGCTC 28

RESULT 2
US-10-136-573A-11
; Sequence 11, Application US/10136573A
; Patent No. US20020161200A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie Rose
; APPLICANT: Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: PI084RIC2
; CURRENT APPLICATION NUMBER: US/10/136,573A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/480,977
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 08/899,437
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 60/052,019
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 11
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-136-573A-11

Query Match 14.2%; Score 55.5; DB 9; Length 45;
Best Local Similarity 35.9%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

Qy 18 FSRCDGRCPNVVVKPLCIKICA---PGCVRLGYL 53
| | | | : : | : | : | | | | |
Db 2 FSRCPKQYKHYC----IKGRCRFVVAEQTPSCVDEGYI 36

RESULT 3
US-09-877-665-11
; Sequence 11, Application US/09877665
; Patent No. US20020164680A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-847-185-47

Query Match 14.2%; Score 55.5; DB 9; Length 45;
Best Local Similarity 35.9%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

Qy 18 FSRCDGRCPNVVVKPLCIKICA---PGCVRLGYL 53
| | | | : : | : | : | | | | |
Db 2 FSRCPKQYKHYC----IKGRCRFVVAEQTPSCVDEGYI 36

RESULT 4
US-10-215-862-11
; Sequence 11, Application US/10215862
; Publication No. US20030036166A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie Rose
; APPLICANT: Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
; TITLE OF INVENTION: Uses Therefor
; FILE REFERENCE: PI084R1D2C1
; CURRENT APPLICATION NUMBER: US/10/215,862
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/126,663
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 08/899,437
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 60/052,019
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 11
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-862-11

Query Match 14.2%; Score 55.5; DB 9; Length 45;
Best Local Similarity 35.9%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

Qy 18 FSRCDGRCPNVVVKPLCIKICA---PGCVRLGYL 53
| | | | : : | : | : | | | | |
Db 2 FSRCPKQYKHYC----IKGRCRFVVAEQTPSCVDEGYI 36

RESULT 5
US-09-817-647-11
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; Sequence 11, Application US/09817647
; Patent No. US20020082229A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; NUMBER OF SEQUENCES: 23
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/817,647
; FILING DATE: 26-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/107,979
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1084R1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: hBPC.efg
; LOCATION: 1-45
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-817-647-11

Query Match 14.2%; Score 55.5; DB 10; Length 45;
Best Local Similarity 35.9%; Pred. No. 31;
Matches 14; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

QY 18 FSRCDGRCQRCPCNVVVKPLCIKICA---PGCVCLGVL 53
||||| : : : : : : : : : : : : : : : : : : : :
Db 2 FSRCPKYKHVC-----IKGRCFVVAEQTPSCVCDGYI 36

RESULT 6
US-09-917-340-73
; Sequence 73, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; TITLE OF INVENTION: HUMAN SOMATOMEDIAN CARRIER PROTEIN SUBUNITS
; TITLE OF INVENTION: AND PROCESS FOR PRODUCING THEM; RECOMBINANT DNA MOLECULES,
; TITLE OF INVENTION: HOSTS, PROCESSES AND HUMAN SOMATOMEDIAN CARRIER PROTEIN-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: TPANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15

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; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-09-917-340-73

Query Match 12.5%; Score 49; DB 10; Length 40;
Best Local Similarity 48.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 42 CAPGCVCR--LGYLRNKKKVCVPRS 64
|| : : : : : : : : : : : : : : : : : : : :
Db 16 CAAHCIARGNRGGYCNKKKVCVCRN 40

RESULT 7
US-09-917-340-68
; Sequence 68, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-68

Query Match 12.3%; Score 48; DB 10; Length 40;
Best Local Similarity 29.4%; Pred. No. 1.5e+02;
Matches 10; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

QY 7 GGRGKCPSEIFSRCDGRCQRCPCNVVVKPLCIK 40
||||| : : : : : : : : : : : : : : : : : : : :
Db 11 GNRGIC----LLNRCPGRMROIGTCLAPRVKCCR 40

RESULT 8
US-09-865-578-4
; Sequence 4, Application US/09865578
; Patent No. US20010034433A1
; GENERAL INFORMATION:
; APPLICANT: E. MARTIN, SPENCER
; TITLE OF INVENTION: HUMAN SOMATOMEDIAN CARRIER PROTEIN SUBUNITS
; TITLE OF INVENTION: AND PROCESS FOR PRODUCING THEM; RECOMBINANT DNA MOLECULES,
; TITLE OF INVENTION: HOSTS, PROCESSES AND HUMAN SOMATOMEDIAN CARRIER PROTEIN-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 057491/0680
; CURRENT APPLICATION NUMBER: US/09/865,578
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/397,192
; PRIOR FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 09/162,118
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: 08/923,860
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 08/706,755
; PRIOR FILING DATE: 1996-09-03

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us-09-506-978-1.slim.rapb

Thu Feb 27 09:12:56 2003

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; PRIOR APPLICATION NUMBER: 08/437,407
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: 08/320,123
; PRIOR FILING DATE: 1994-10-07
; PRIOR APPLICATION NUMBER: 08/043,039
; PRIOR FILING DATE: 1993-04-05
; PRIOR APPLICATION NUMBER: 07/763,481
; PRIOR FILING DATE: 1991-09-20
; PRIOR APPLICATION NUMBER: 07/290,250
; PRIOR FILING DATE: 1988-12-22
; PRIOR APPLICATION NUMBER: 07/170,022
; PRIOR FILING DATE: 1988-03-31
; PRIOR APPLICATION NUMBER: 07/034,885
; PRIOR FILING DATE: 1987-04-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Gly or Ala
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: Phe or Glu
; US-09-865-578-4

Query Match          12.1%; Score 47.5; DB 10; Length 42;
Best Local Similarity 32.7%; Pred. No. 1.7e+02;
Matches 16; Conservative 2; Mismatches 14; Indels 17; Gaps 4;

QY 5 GLGGRGKCPSEIFSRCDGRCQFCPNVVPKPLCIKICA-----PGCVC 48
    ||| :| ||| | | | | | | | | | | | | | | | | | | |
Db 6 GLGVPVRC-----XPCDARALAQ-----APPP-----AVCAELVREPCCGC 42

RESULT 9
US-09-864-761-44588
; Sequence 44588, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

Query Match          12.1%; Score 47.5; DB 10; Length 42;
Best Local Similarity 32.7%; Pred. No. 1.7e+02;
Matches 16; Conservative 2; Mismatches 14; Indels 17; Gaps 4;

QY 5 GLGGRGKCPSEIFSRCDGRCQFCPNVVPKPLCIKICA-----PGCVC 48
    ||| :| ||| | | | | | | | | | | | | | | | | | | |
Db 6 GLGVPVRC-----XPCDARALAQ-----APPP-----AVCAELVREPCCGC 42

RESULT 10
US-09-829-481-11
; Sequence 11, Application US/09829481
; Patent No. US20020069427A1
; GENERAL INFORMATION:
; APPLICANT: Presnail, James
; APPLICANT: Weng, Zude
; APPLICANT: Wong, James
; TITLE OF INVENTION: Arthropod Defensins
; FILE REFERENCE: BB1441 US NA
; CURRENT APPLICATION NUMBER: US/09/829,481
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/197279
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Androctonus australis hector
; US-09-829-481-11

Query Match          11.8%; Score 46; DB 10; Length 37;
Best Local Similarity 27.1%; Pred. No. 2.1e+02;
Matches 13; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY 2 GFGLGGRGKCPSEIFSRCDGRCQFCPNVVPK-PLCIKICAPGVC 48
    ||| ||| | | | | | | | | | | | | | | | | | | |
Db 1 GFG-----CPFNQ-----GACHRHCRSIRRRGGYCAGLFKQTC 35

RESULT 11
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US-09-917-340-57
; Sequence 57, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Christopher J.
; APPLICANT: McAnulty, Jonathan F.
; APPLICANT: Reid, Ted W.
; TITLE OF INVENTION: Transplant Media
; FILE REFERENCE: TPLANT-06468
; CURRENT APPLICATION NUMBER: US/09/917,340
; CURRENT FILING DATE: 2001-07-29
; PRIOR APPLICATION NUMBER: 60/221,632
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/249,602
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/290,932
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Androctonus Australis Hector
US-09-917-340-57

Query Match      11.8%; Score 46; DB 10; Length 37;
Best Local Similarity 27.1%; Pred. No. 2.1e+02;
Matches 13; Conservative 5; Mismatches 16; Indels 14; Gaps 3;

QY  2 GFGGLGGRGKCPSEIFSRCDGRCPNVPK-PLCIKICAPGVCV 48
    ||| ||| : ||| : ||| : ||| : ||| : ||| : |||
Db   1 GFG-----CPFNQ-----GACHRHRSIRRRGGYCAGLRFKQTCTC 35

RESULT 12
US-10-136-573A-13
; Sequence 13, Application US/10136573A
; Patent No. US20020161200A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie Rose
; APPLICANT: Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
; FILE REFERENCE: P1084R1C2
; CURRENT APPLICATION NUMBER: US/10/136,573A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/480,977
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 08/899,437
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 60/052,019
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 13
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-136-573A-13

Query Match      11.5%; Score 45; DB 9; Length 45;
Best Local Similarity 34.6%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

QY  35 KPICI-----KICAPGCVRLGY 52
    | || : ||| : ||| : ||| : |||
Db   10 KDFCIHGECKYVKELRAPSCICHPGY 35

RESULT 13
US-09-877-665-13
; Sequence 13, Application US/09877665
; Patent No. US20020164680A1
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; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
;                               Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,665
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,206
; FILING DATE: 30-Jun-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487
; REFERENCE/DOCKET NUMBER: P1084R1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-2066
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; TYPE: Amino Acid
; LENGTH: 45 amino acids
; TOPOLOGY: Linear
; FEATURE:
; NAME/KEY: hHB-EGF.egf
; LOCATION: 1-45
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-877-665-13

Query Match      11.5%; Score 45; DB 9; Length 45;
Best Local Similarity 34.6%; Pred. No. 3.2e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

QY  35 KPICI-----KICAPGCVRLGY 52
    | || : ||| : ||| : ||| : |||
Db   10 KDFCIHGECKYVKELRAPSCICHPGY 35

RESULT 14
US-10-215-862-13
; Sequence 13, Application US/10215862
; Publication NO. US20030036166A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie Rose
; APPLICANT: Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
; FILE REFERENCE: P1084R1D2C1
; CURRENT APPLICATION NUMBER: US/10/215,862
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: US 09/126,663
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 08/899,437
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 60/052,019
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
```



```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124,557
; FILING DATE: 16-Apr-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/643,502
; FILING DATE: 18-JAN-1991
; APPLICATION NUMBER: US 07/546,114
; FILING DATE: 29-JUN-1990
; APPLICATION NUMBER: US 07/457,196
; FILING DATE: 29-DEC-1989
; APPLICATION NUMBER: US 07/390,901
; FILING DATE: 08-AUG-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cseri, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: GI 5190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)876-1170
; TELEFAX: (617)876-5851
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
;
; US-10-124-557-8
;
; Query Match 11.3%; Score 44; DB 12; Length 40;
; Best Local Similarity 32.4%; Pred. No. 3.6e+02;
; Matches 11; Conservative 7; Mismatches 6; Indels 10; Gaps 3;
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; QY 6 LGGRGKCPSEIFSR-----CDGRQCF---CPN 31
; Db 2 LSCGRC--PESFERGECDAQCKKDKCCPD 33
;
; RESULT 19
; US-09-814-452-5
; Sequence 5, Application US/09814452
; Publication No. US20020197689A1
; GENERAL INFORMATION:
; APPLICANT: CORZO, GERARDO
; APPLICANT: ESCOBAS, PIERRE
; TITLE OF INVENTION: INSECTICIDAL PEPTIDES AND METHODS FOR USE OF SAME
; FILE REFERENCE: 16313-0028
; CURRENT APPLICATION NUMBER: US/09/814,452
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/191,380
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Xysticus acerbus
;
; US-09-814-452-5
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; Query Match 11.1%; Score 43.5; DB 9; Length 37;
; Best Local Similarity 30.4%; Pred. No. 3.7e+02;

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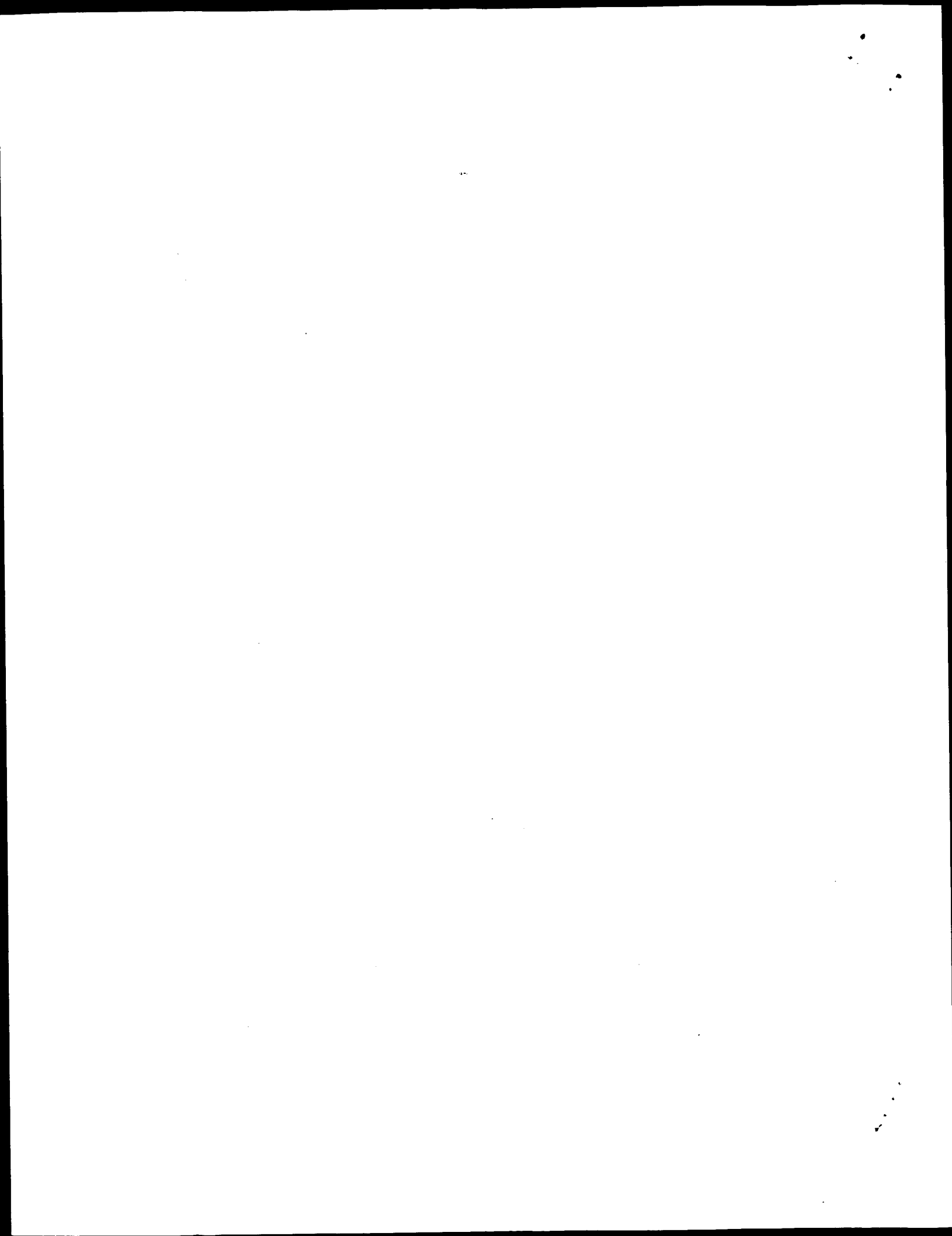
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; Matches 14; Conservative 4; Mismatches 13; Indels 15; Gaps 3;
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; QY 6 LGGRGKCPSEIFSR---CDGRQCFPNVVPKPLCIKICAPGCV 48
; Db 3 IGGGGC---SVFSGPCCGCTCKCKFVLPK-----GCHC 36
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; RESULT 20
; US-10-136-573A-16
; Sequence 16, Application US/10136573A
; Patent No. US20020161200A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie Rose
; APPLICANT: Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
; FILE REFERENCE: P1084R1C2
; CURRENT APPLICATION NUMBER: US/10/136,573A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 09/480,977
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 08/899,437
; PRIOR FILING DATE: 1997-07-24
; PRIOR APPLICATION NUMBER: US 60/052,019
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 16
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
;
; US-10-136-573A-16
;
; Query Match 11.1%; Score 43.5; DB 9; Length 45;
; Best Local Similarity 30.6%; Pred. No. 4.4e+02;
; Matches 11; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
;
; QY 18 FSRCDGRCQRCFPNVVPKPLCIKICAPGCVCRGLYL 53
; Db 2 FNDPCDSHTQCFPHGTCTFL-VOEDKPCACVCHGYV 36
;
; RESULT 21
; US-09-877-665-16
; Sequence 16, Application US/09877665
; Patent No. US20020164680A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
; Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/877,665
; FILING DATE: 08-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/109,206
; FILING DATE: 30-Jun-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Conley, Deirdre L.
; REGISTRATION NUMBER: 36,487

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Job time : 14 secs



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OM protein - protein search, using sw model

Run on: February 27, 2003, 09:03:05 ; Search time 29 Seconds  
(without alignments)  
67.977 Million cell updates/sec

Title: US-09-506-978-1

Perfect score: 391

Sequence: 1 GGGGILGGKGRKCPSEIFSR.....CRLGYLRNKKVKCVPRSKG 67

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 17865

Minimum DB seq length: 32

Maximum DB seq length: 45

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2.6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2.6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2.6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2.6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2.6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55.5	14.2	38	2	US-08-902-516-47
2	55.5	14.2	45	3	US-08-899-437-11
3	55.5	14.2	45	4	US-09-126-121-11
4	52.5	13.4	44	6	5177197-48
5	52	13.3	42	2	US-08-761-248B-15
6	51	13.0	32	2	US-08-384-714-4
7	51	13.0	39	6	5258287-56
8	50	12.8	32	1	US-08-425-069-44
9	50	12.8	32	2	US-08-317-844B-44
10	49.5	12.7	33	1	US-08-682-485A-24
11	49.5	12.7	33	1	US-08-451-472-7
12	49.5	12.7	33	2	US-08-933-314-24
13	49	12.5	42	4	US-09-284-819-1
14	48.5	12.4	42	1	US-08-278-089A-20
15	48	12.3	40	1	US-08-033-873-10
16	48	12.3	40	2	US-08-356-832-10
17	48	12.3	40	4	US-08-988-705-10
18	47.5	12.1	43	4	US-09-230-196-19
19	47	12.0	39	2	US-08-535-494-5
20	47	12.0	39	4	US-09-097-635-5
21	47	12.0	45	1	US-08-608-786-2
22	47	12.0	45	2	US-08-824-382-2
23	46.5	11.9	38	4	US-09-384-302A-14
24	46	11.8	33	1	US-08-425-069-7
25	46	11.8	33	2	US-08-317-844B-7
26	46	11.8	37	1	US-08-212-236-10
27	45.5	11.6	43	1	US-08-179-481-81

28	45	11.5	32	2	US-08-384-714-5	Sequence 5, Appli
29	45	11.5	39	1	US-08-212-236-4	Sequence 4, Appli
30	45	11.5	39	4	US-09-228-302-11	Sequence 11, Appli
31	45	11.5	41	1	US-08-168-091A-41	Sequence 41, Appli
32	45	11.5	45	2	US-08-838-763-3	Sequence 3, Appli
33	45	11.5	45	2	US-08-838-763-7	Sequence 7, Appli
34	45	11.5	45	2	US-08-838-763-8	Sequence 8, Appli
35	45	11.5	45	3	US-08-719-500-1	Sequence 1, Appli
36	45	11.5	45	3	US-08-899-437-13	Sequence 13, Appli
37	45	11.5	45	4	US-09-126-121-13	Sequence 13, Appli
38	44	11.3	32	2	US-08-384-714-8	Sequence 8, Appli
39	44	11.3	34	1	US-08-425-069-42	Sequence 42, Appli
40	44	11.3	34	1	US-08-425-069-52	Sequence 52, Appli
41	44	11.3	34	1	US-08-425-069-54	Sequence 54, Appli
42	44	11.3	34	2	US-08-317-844B-42	Sequence 42, Appli
43	44	11.3	34	2	US-08-317-844B-54	Sequence 54, Appli
44	44	11.3	40	4	US-07-757-022B-8	Sequence 8, Appli
45	44	11.3	43	4	US-09-230-637-61	Sequence 61, Appli
46	44	11.3	45	1	US-08-244-113-2	Sequence 2, Appli
47	44	11.3	45	1	US-08-980-858A-18	Sequence 18, Appli
48	43.5	11.1	35	3	US-08-980-858A-42	Sequence 42, Appli
49	43.5	11.1	35	3	US-08-980-858A-42	Sequence 42, Appli
50	43.5	11.1	41	1	US-08-168-091A-45	Sequence 45, Appli

## ALIGNMENTS

RESULT 1  
US-08-902-516-47  
; Sequence 47, Application US/08902516  
; Patent No. 5891432  
; GENERAL INFORMATION:  
; APPLICANT: Soo Hoo, William  
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS  
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE  
; NUMBER OF SEQUENCES: 50  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL & FLORES, LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,516  
; FILING DATE: 29-JUL-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IM 2442  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)535-9001  
; TELEFAX: (619)535-8949  
; INFORMATION FOR SEQ ID NO: 47:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-902-516-47

Query Match 14.2%; Score 55.5; DB 2; Length 38;  
Best Local Similarity 29.8%; Pred. No. 18;  
Matches 14; Conservative 0; Mismatches 14; Indels 19; Gaps 2;



ADDRESSEE: Jenkins & Gilchrist  
STREET: 1100 Louisiana, Suite 1800  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77002  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/761.248B  
FILING DATE: 06-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/008,348  
FILING DATE: 07-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Turley, Charles P  
REGISTRATION NUMBER: 35,723  
REFERENCE/DOCKET NUMBER: 34012.6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (713)9513310  
TELEFAX: (713)9513314  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 42 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-761-248B-15

Query Match 13.3%; Score 52; DB 2; Length 42;  
Best Local Similarity 35.0%; Pred. No. 45;  
Matches 14; Conservative 2; Mismatches 20; Indels 4; Gaps 2;

QY 12 CPSNEIFSRCDGRCQFCFNVVPPKPLKICAPGC--VCR 49  
DB 1 CPKNP--PRSIGTCVELSGDQSCPNIOKCSNGCGHCK 38

RESULT 6  
US-08-384-714-4  
Sequence 4, Application US/08384714  
Patent No. 5840687  
GENERAL INFORMATION:  
APPLICANT: Harkins, Richard  
APPLICANT: Seto, Marian  
APPLICANT: Katz, Bradley  
TITLE OF INVENTION: MODIFIED LIGANDS FOR RECEPTOR TYROSINE  
TITLE OF INVENTION: KINASES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wendy L. Washtien  
STREET: 15049 San Pablo Avenue  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804-0099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/384.714  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Washtien, Wendy L.

REGISTRATION NUMBER: 36,301  
REFERENCE/DOCKET NUMBER: A-0108  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-262-5411  
TELEFAX: 510-262-7095  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-384-714-4

Query Match 13.0%; Score 51; DB 2; Length 32;  
Best Local Similarity 50.0%; Pred. No. 44;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 38 CIKICAPGCVCRGLYL 53  
DB 6 CFHGTSPGCVCHSGYV 21

RESULT 7  
5258287-56  
Patent No. 5258287  
APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.  
TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION  
OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53  
NUMBER OF SEQUENCES: 58  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/171,623  
FILING DATE: 22-MAR-1988  
SEQ ID NO: 56  
LENGTH: 39  
5258287-56

Query Match 13.0%; Score 51; DB 6; Length 39;  
Best Local Similarity 32.6%; Pred. No. 53;  
Matches 14; Conservative 3; Mismatches 18; Indels 8; Gaps 2;

QY 4 GGLGRCCKPSNEIFSRCDGRCQFCFNVVPPKPLKICAPGC 46  
DB 5 GGLGPPVVR-----EPCDARALAQ--APPVAVCELVREPGC 39

RESULT 8  
US-08-425-069-44  
Sequence 44, Application US/08425069  
Patent No. 5728810  
GENERAL INFORMATION:  
APPLICANT: Lewis, Randolph V.  
APPLICANT: Xu, Ming  
APPLICANT: Himman, Michael B.  
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK  
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF  
NUMBER OF SEQUENCES: 69  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 No. 5728810th Washington Street  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/425,069  
FILING DATE: 19-APR-1995  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-106P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX:  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: nephila clavipes  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..32  
OTHER INFORMATION: /label= silk1\_repeat  
US-08-425-069-44

Query Match 12.8%; Score 50; DB 1; Length 32;  
Best Local Similarity 80.0%; Pred. No. 56;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFGLGGRG 10  
||:|||||:|  
Db 23 GGYGLGGQ 32

## RESULT 9

US-08-317-844B-44  
Sequence 44, Application US/08317844B  
Patent No. 5989894

GENERAL INFORMATION:  
APPLICANT: Lewis, Randolph V.  
APPLICANT: Xu, Ming  
APPLICANT: Himan, Michael B.  
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK  
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 301 No. 5989894th Washington Street  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,844B  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1447-105P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 241-1300  
TELEFAX: (703) 241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids

TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: nephila clavipes  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..32  
OTHER INFORMATION: /label= silk1\_repeat  
US-08-317-844B-44

Query Match 12.8%; Score 50; DB 2; Length 32;  
Best Local Similarity 80.0%; Pred. No. 56;  
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGFGLGGRG 10  
||:|||||:|  
Db 23 GGYGLGGQ 32

## RESULT 10

US-08-682-485A-24  
Sequence 24, Application US/08682485A  
Patent No. 5763568

GENERAL INFORMATION:  
APPLICANT: ATKINSON, RONALD K  
APPLICANT: HOWDEN, MERLIN E.H.  
APPLICANT: TYLER, MARGARET I  
APPLICANT: VONARX, EDWARD J  
TITLE OF INVENTION: Insecticidal Toxins Derived From  
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zeneca, Inc.  
STREET: 1200 South 47th Street  
CITY: Richmond  
STATE: California  
COUNTRY: USA  
ZIP: 94804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485A  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/682,485  
FILING DATE: 17-JULY-1996  
APPLICATION NUMBER: US/08/256,933  
FILING DATE: 27-JULY-1994  
APPLICATION NUMBER: WO 93/15108  
FILING DATE: 29-JAN-1993  
APPLICATION NUMBER: AU PL0722  
FILING DATE: 31-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Shaw, Melissa A.  
REGISTRATION NUMBER: 38,301  
REFERENCE/DOCKET NUMBER: PPD 5099/D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-231-1542  
TELEFAX: 510-231-1112  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

RESULT 12  
US-08-933-314-24  
; Sequence 24, Application US/08933314  
; Patent No. 5959182  
; GENERAL INFORMATION:  
; APPLICANT: ATKINSON, RONALD K

/ APPLICANT: THE Government of the United States of America  
 / APPLICANT: as represented by The Secretary of the  
 / APPLICANT: Department of Health and Human Services  
 / TITLE OF INVENTION: Methods and Compositions for Inhibiting Inflammation  
 / TITLE OF INVENTION: and Angiogenesis Comprising a Mammalian CD97 Alpha  
 / TITLE OF INVENTION: Subunit  
 / FILE REFERENCE: 015280-26310005  
 / CURRENT APPLICATION NUMBER: US/09/284.819





COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/356,832  
FILING DATE: 12-DEC-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/033,873  
FILING DATE: 19-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: CAMPBELL, CATHRYN A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UC 9552  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-356-832-10

Query Match 12.3%; Score 48; DB 2; Length 40;  
Best Local Similarity 29.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

Qy 7 GGRGKCPSEIFSRCDGRQRCPCNVVVKPLCIK 40  
Db 11 GNRGIC----LLNRCPGRMRQIGTCLAPRVKCCR 40

RESULT 17  
US-08-988-705-10  
Sequence 10, Application US/08988705  
Patent No. 6211148  
GENERAL INFORMATION:  
APPLICANT: Selted, Michael E.  
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE  
TITLE OF INVENTION: NEUTROPHILS  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL & FLORES, LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,705  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/033,873  
FILING DATE: 19-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356,832  
FILING DATE: 13-DEC-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UC 2918  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)535-9001  
TELEFAX: (619)535-8949  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-988-705-10

Query Match 12.3%; Score 48; DB 4; Length 40;  
Best Local Similarity 29.4%; Pred. No. 1.1e+02;  
Matches 10; Conservative 7; Mismatches 13; Indels 4; Gaps 1;

Qy 7 GGRGKCPSEIFSRCDGRQRCPCNVVVKPLCIK 40  
Db 11 GNRGIC----LLNRCPGRMRQIGTCLAPRVKCCR 40

RESULT 18  
US-09-230-196-19  
Sequence 19, Application US/09230196  
Patent No. 6307035  
GENERAL INFORMATION:  
APPLICANT: Rauscher III, Frank J.  
APPLICANT: Jensen, David E.  
TITLE OF INVENTION: BRCA1 Associated Protein (BAP-1) and  
TITLE OF INVENTION: Uses Therefor  
NUMBER OF SEQUENCES: 47  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howson and Howson  
STREET: Spring House Corporate Cntr., PO Box 457  
CITY: Spring House  
STATE: Pennsylvania  
COUNTRY: U.S.A.  
ZIP: 19477  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/230,196  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/022,997  
FILING DATE: 02-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/038,109  
FILING DATE: 19-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Bak, Mary E.  
REGISTRATION NUMBER: 31,215  
REFERENCE/DOCKET NUMBER: WST688USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-540-9200  
TELEFAX: 215-540-5818  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-230-196-19

Query Match 12.1%; Score 47.5; DB 4; Length 43;  
Best Local Similarity 42.1%; Pred. No. 1.3e+02;  
Matches 8; Conservative 5; Mismatches 5; Indels 1; Gaps 1;

Qy 24 RCORCPNVVVKPLCIK 42  
Db 11 GNRGIC----LLNRCPGRMRQIGTCLAPRVKCCR 40

Db 3 RCSR-CTNILREPVLGGC 20

## RESULT 19

US-08-535-494-5  
; Sequence 5, Application US/08535494  
; Patent No. 5861275  
; GENERAL INFORMATION:

APPLICANT: HANSEN, J. N.  
TITLE OF INVENTION: LANTIBIOTIC MUTANTS AND CHIMERAS OF  
; TITLE OF INVENTION: ENHANCED STABILITY AND ACTIVITY, LEADER SEQUENCES  
; THEREFOR, GENES ENCODING THE SAME, AND METHODS OF  
; TITLE OF INVENTION: THEREFOR, GENES ENCODING THE SAME, AND METHODS OF  
; TITLE OF INVENTION: PRODUCING AND USING THE SAME  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,494

FILING DATE: 28-SEP-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 2747-066-0

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-535-494-5

Query Match 12.0%; Score 47; DB 2; Length 39;  
Best Local Similarity 43.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 32 VVPRPLCIKICAPGV 47

Db 4 ITPQITSISLCTPGCV 19

## RESULT 20

US-09-097-635-5  
; Sequence 5, Application US/09097635  
; Patent No. 6153405  
; GENERAL INFORMATION:

APPLICANT: HANSEN, J. N.  
TITLE OF INVENTION: LANTIBIOTIC MUTANTS AND CHIMERAS OF  
; TITLE OF INVENTION: ENHANCED STABILITY AND ACTIVITY, LEADER SEQUENCES  
; THEREFOR, GENES ENCODING THE SAME, AND METHODS OF  
; TITLE OF INVENTION: THEREFOR, GENES ENCODING THE SAME, AND METHODS OF  
; TITLE OF INVENTION: PRODUCING AND USING THE SAME  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/535,494

FILING DATE: 28-SEP-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 2747-066-0

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-097-635-5

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/097,635  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/535,494

FILING DATE: 28-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 2747-066-0

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-097-635-5

Query Match 12.0%; Score 47; DB 4; Length 39;  
Best Local Similarity 43.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 32 VVPRPLCIKICAPGV 47

Db 4 ITPQITSISLCTPGCV 19

## RESULT 21

US-08-608-786-2

; Sequence 2, Application US/08608786

; Patent No. 5703049

; GENERAL INFORMATION:

APPLICANT: Rao, A. Gururaj

TITLE OF INVENTION: High Methionine Derivatives of

TITLE OF INVENTION: Alpha-Hordothionin for Pathogen-Control

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pioneer Hi-Bred International, Inc.

STREET: 700 Capital Square, 400 Locust Street

CITY: Des Moines

STATE: Iowa

COUNTRY: United States of America

ZIP: 50309

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/608,786

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Simon, Soma G.

REGISTRATION NUMBER: 37,444

REFERENCE/DOCKET NUMBER: 456-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-248-4896

TELEFAX: 515-248-4844

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids

TYPE: amino acid

TOPOLOGY: linear  
US-08-608-786-2

Query Match 12.0%; Score 47; DB 1; Length 45;  
Best Local Similarity 31.2%; Pred. No. 1.6e+02;  
Matches 10; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 19 SRCDCRCQFCPNVVPKPLCIKICAPGCVCRLL 50  
| | | | | : | | | | | : | | | | | : | | | | | :  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 2 SCCRSTMGRCMYNMCRCMRGAMKILCAGVCRCMK 33

## RESULT 22

US-08-824-382-2  
; Sequence 2, Application US/08824382  
; Patent No. 5885802

## GENERAL INFORMATION:

APPLICANT: Rao, A. Gururaj  
TITLE OF INVENTION: High Methionine Derivatives of  
Alpha-Hordothionin  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pioneer Hi-Bred International, Inc.  
STREET: 700 Capital Square, 400 Locust Street  
CITY: Des Moines

STATE: Iowa

COUNTRY: United States of America

ZIP: 50309

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/824,382

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/460,440

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Simon, Soma G.

REGISTRATION NUMBER: 37,444

REFERENCE/DOCKET NUMBER: 355-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-248-4896

TELEFAX: 515-248-4844

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-824-382-2

Query Match 12.0%; Score 47; DB 2; Length 45;  
Best Local Similarity 31.2%; Pred. No. 1.6e+02;  
Matches 10; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 19 SRCDCRCQFCPNVVPKPLCIKICAPGCVCRLL 50  
| | | | | : | | | | | : | | | | | : | | | | | :  
| | | | | : | | | | | : | | | | | : | | | | | :  
DB 2 SCCRSTMGRCMYNMCRCMRGAMKILCAGVCRCMK 33

## RESULT 23

US-09-384-302A-14

; Sequence 14, Application US/09384302A

; Patent No. 6451543

## GENERAL INFORMATION:

APPLICANT: kochendoerfer, Gerd G

APPLICANT: Hunter, Christle L

APPLICANT: Kent, Stephen B.H.

APPLICANT: Botti, Paolo

APPLICANT: Gryphon Sciences

; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis  
; TITLE OF INVENTION: of Membrane Polypeptides  
; FILE REFERENCE: grfn-028/02WO  
; CURRENT APPLICATION NUMBER: US/09/384,302A  
; CURRENT FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: 09/144,964  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 09/263,971  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 38  
; TYPE: PRI  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-384-302A-14

Query Match 11.9%; Score 46.5; DB 4; Length 38;  
Best Local Similarity 39.3%; Pred. No. 1.5e+02;  
Matches 11; Conservative 3; Mismatches 13; Indels 1; Gaps 1;

QY 36 PLCIKICAPGCVCRLLGYLRNKKKVCVPR 63  
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| | | | | : | | | | | : | | | | | : | | | | | :  
DB 12 PQCIKPKCDAGM-RFGKCMNRKCHCTPK 38

## RESULT 24

US-08-425-069-7

; Sequence 7, Application US/08425069

; Patent No. 5728810

## GENERAL INFORMATION:

APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL  
CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch

STREET: 301 No. 5728810th Washington Street

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22046

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,069

FILING DATE: 19-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1447-106P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

TELEX:

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Nephila clavipes

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FEATURE:
NAME/KEY: Peptide
LOCATION: 1..33
OTHER INFORMATION: /label= repeat_unit
OTHER INFORMATION: /note= "The protein of the present invention is
OTHER INFORMATION: constituted primarily of repeats of this
OTHER INFORMATION: sequence."
FEATURE:
NAME/KEY: Region
LOCATION: 13..18
OTHER INFORMATION: /label= alanine_stretch
OTHER INFORMATION: /note= "This run of alanine residues can also have
OTHER INFORMATION: 7 residues."
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 6
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 9
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 26
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
US-08-425-069-7
Query Match 11.8%; Score 46; DB 1; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGFGGLGGRG 10
Db 24 GXGGLGGQG 33
RESULT 25
US-08-317-844B-7
Sequence 7, Application US/08317844B
Patent No. 5989894
GENERAL INFORMATION:
APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: PROTEIN, A REPLICABLE VECTOR AND A TRANSFORMED CELL
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS THEREOF
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESS: Birch, Stewart, Kolasch & Birch
STREET: 301 No. 5989894th Washington Street
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22046
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,844B
FILING DATE: 04-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
```

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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Nephila clavipes
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..33
OTHER INFORMATION: /label= repeat_unit
OTHER INFORMATION: /note= "The protein of the present invention is
OTHER INFORMATION: constituted primarily of repeats of this
OTHER INFORMATION: sequence."
FEATURE:
NAME/KEY: Region
LOCATION: 13..18
OTHER INFORMATION: /label= alanine_stretch
OTHER INFORMATION: /note= "This run of alanine residues can also have
OTHER INFORMATION: 7 residues."
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 6
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 9
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
FEATURE:
NAME/KEY: Variable amino acid
LOCATION: 26
OTHER INFORMATION: /label= modified_a.a.
OTHER INFORMATION: /note= "This residue can be leucine, tyrosine or
OTHER INFORMATION: glutamine"
US-08-317-844B-7
Query Match 11.8%; Score 46; DB 2; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGFGGLGGRG 10
Db 24 GXGGLGGQG 33
Search completed: February 27, 2003, 09:05:41
Job time : 30 secs
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